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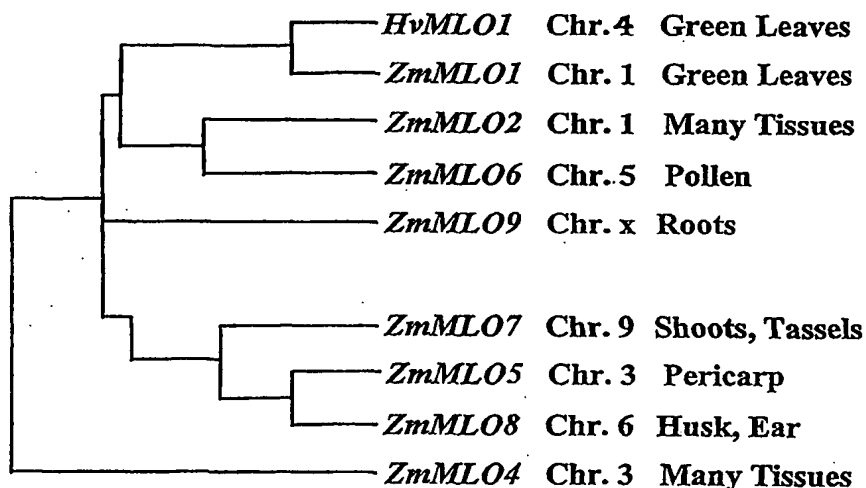


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(54) Title: MANIPULATION OF *MLO* GENES TO ENHANCE DISEASE RESISTANCE IN PLANTS

Maize *MLO* Resistance Gene Homologues



(57) Abstract

Compositions and methods for enhancing disease resistance in plants are provided. The method involves modulating the activity of *Mlo* sequences in the plant. Particular *Mlo* sequences are provided that can be manipulated to enhance pathogen resistance in modified plants. Transformed plants, plant cells, tissues, and seed are also provided having enhanced disease resistance.

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MANIPULATION OF *MLO* GENES  
TO ENHANCE DISEASE RESISTANCE IN PLANTS

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FIELD OF THE INVENTION

The invention relates to the genetic manipulation of plants, particularly to transforming plants with genes that enhance disease resistance.

BACKGROUND OF THE INVENTION

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Disease in plants is caused by biotic and abiotic causes. Biotic causes include fungi, viruses, bacteria, and nematodes. Of these, fungi are the most frequent causative agent of disease on plants. Abiotic causes of disease in plants include extremes of temperature, water, oxygen, soil pH, plus nutrient-element deficiencies and imbalances, excess heavy metals, and air pollution.

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A host of cellular processes enables plants to defend themselves from disease caused by pathogenic agents. These processes apparently form an integrated set of resistance mechanisms that is activated by initial infection and then limits further spread of the invading pathogenic microorganism. This limitation of the pathogen intruder is frequently accomplished by localized containment of the intruder following a coordinated complex defense response.

20

Subsequent to recognition of a potentially pathogenic microbe, plants can activate an array of biochemical responses. Generally, the plant responds by inducing several local responses in the cells immediately surrounding the infection site. The most common resistance response observed in both nonhost and race-specific interactions is termed the "hypersensitive response" (HR). In the hypersensitive response, cells contacted by the pathogen, and often neighboring cells, rapidly collapse and dry in a necrotic fleck. Other responses include the deposition of callose, the physical thickening of cell walls by lignification, and the synthesis of various antibiotic small molecules and proteins. Genetic factors in both the host and the pathogen determine the specificity of these local responses, which can be very effective in limiting the spread of infection.

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The hypersensitive response in many plant-pathogen interactions is specified by and dependent on the presence of two complementary genes, one from the host and one from the pathogen. These complementary genes are the resistance (*R*) gene in the plant and a corresponding avirulence (*avr*) gene in the pathogen. The interaction of the genes is associated with the rapid, localized cell death of the hypersensitive response. *R* genes that respond to specific bacterial, fungal, or viral pathogens, have been isolated from a variety of plant species and several appear to encode cytoplasmic proteins.

The resistance gene in the plant and the avirulence gene in the pathogen often conform to a gene-for-gene relationship. That is, resistance to a pathogen is only observed when the pathogen carries a specific avirulence gene and the plant carries a corresponding or complementing resistance gene. Because *avr-R* gene-for-gene relationships are observed in many plant-pathogen systems and are accompanied by a characteristic set of defense responses, a common molecular mechanism underlying *avr-R* gene mediated resistance has been postulated. A simple model which has been proposed is that pathogen *avr* genes directly or indirectly generate a specific molecular signal (ligand) that is recognized by cognate receptors encoded by plant *R* genes.

Both plant resistance genes and corresponding pathogen avirulence genes have been cloned. The plant kingdom contains thousands of *R* genes with specific specificities for viral, bacterial, fungal, or nematode pathogens. Although there are differences in the defense responses induced during different plant-pathogen interactions, some common themes are apparent among *R* gene-mediated defenses. The function of a given *R* gene is dependent on the genotype of the pathogen. Plant pathogens produce a diversity of potential signals, and in a fashion analogous to the production of antigens by mammalian pathogens, some of these signals are detectable by some plants.

The avirulence gene causes the pathogen to produce a signal that triggers a strong defense response in a plant with the appropriate *R* gene. However, expressing an avirulence gene does not stop the pathogen from being virulent on hosts that lack the corresponding *R* gene. A single plant can have many *R* genes, and a pathogen can have many *avr* genes.

Monogenic resistance mediated by recessive (*mlo*) alleles of the *Mlo* locus is different. It differs from race-specific incompatibility to single pathogen strains in that it is believed to confer a broad spectrum resistance to almost all known isolates of the fungal pathogen, and the resistance is

5 apparently durable in the field despite extensive cultivation. Further, *mlo* resistance alleles have been obtained by mutagen treatment of susceptible wild-type *Mlo* varieties. These *mlo* plants exhibit a spontaneous leaf cell death phenotype under pathogen-free or even axenic conditions.

As noted, among the causative agents of infectious disease of crop

10 plants, the phytopathogenic fungi play the dominant role. Phytopathogenic fungi cause devastating epidemics, as well as causing significant annual crop yield losses. All of the approximately 300,000 species of flowering plants are attacked by pathogenic fungi. However, a single plant species can be host to only a few fungal species, and similarly, most fungi usually have a limited host

15 range.

Plant disease outbreaks have resulted in catastrophic crop failures that have triggered famines and caused major social change. Generally, the best strategy for plant disease control is to use resistant cultivars selected or developed by plant breeders for this purpose. However, the potential for serious

20 crop disease epidemics persists today, as evidenced by outbreaks of the Victoria blight of oats and southern corn leaf blight.

Accordingly, molecular methods are needed to supplement traditional breeding methods to protect plants from pathogen attack. Particularly, methods are needed for broad spectrum resistance to pathogens.

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## SUMMARY OF THE INVENTION

Compositions and methods for creating or enhancing resistance to plant pests are provided. The method provides control of pathogens by modulating the expression of *Mlo* genes. Novel *Mlo* sequences are provided from maize.

- 5 Such sequences can be utilized to modulate the expression of *Mlo* genes in plants, particularly maize, to enhance resistance to pathogens. Generally, such modulation will result in decreased or increased expression of native *Mlo* genes, preferably decreased expression. Such decreased expression can be effected by mutagenesis or expression of modified or antisense *Mlo* sequences described  
10 herein.

- It is recognized that a variety of promoters will be useful in the invention the choice of which will depend in part upon the desired level of expression of the modified sequences in the plant or alternatively, in the plant organ. It is recognized that the levels of expression can be controlled to induce  
15 broad spectrum resistance resulting in levels of immunity in the plant or to induce cell death.

- The methods of the invention find use in controlling plant pests, including fungal pathogens, viruses, nematodes, insects, and the like. Transformed plants and seeds, as well as methods for making such plants and  
20 seeds are additionally provided.

## BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides a sequence alignment for the maize *Mlo* homologues with the barley *Mlo* sequence. The barley sequence is designated as Hv*Mlo*1.

- 25 Figure 2 groups the *Mlo* sequences based on relatedness as well as the plant tissue from which it was isolated.

Figure 3 schematically illustrates a plasmid vector comprising the Zm*Mlo*1 antisense construct operably linked to the ubiquitin promoter.

## DETAILED DESCRIPTION OF THE INVENTION

Compositions of the invention include eight mutation-induced recessive alleles of maize set forth in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13 and 15. The maize sequences exhibit homology to the *Mlo* barley sequence (SEQ ID NO: 5 17). See, Büschges *et al.* (1997) 88:695-705 and Tables 1 and 2. The isolated maize *Mlo* genes are involved in enhancing resistance to plant pests. In particular, the present invention provides for isolated nucleic acid molecules comprising nucleotide sequences encoding the amino acid sequences shown in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, or the nucleotide sequences encoding 10 the DNA sequences deposited in a bacterial host with the American Type Culture Collection and assigned the Accession Nos. 98725, 98726, 98727, 98728, 98729 (SEQ ID NOS: 3, 5, 9, 11, 13 respectively). Further provided are polypeptides having an amino acid sequence encoded by a nucleic acid molecule described herein, for example those set forth in SEQ ID NOS: 1, 5, 3, 15 7, 9, 11, 13, and 15, those deposited with the American Type Culture Collection and assigned Accession Nos. 98725, 98726, 98727, 98728, 98729 (SEQ ID NOS: 3, 5, 9, 11, 13 respectively), and fragments and variants thereof.

Plasmids containing the nucleotide sequences of the invention were deposited with American Type Culture Collection, Manassas, Virginia, and 20 assigned Accession Nos. 98725, 98726, 98727, 98728, 98729 (SEQ ID NOS: 3, 5, 9, 11, 13 respectively). These deposits will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. These deposits were made merely as a convenience for those of skill in the art and are not an 25 admission that a deposit is required under 35 U.S.C. §112.

The invention encompasses isolated or substantially purified nucleic acid or protein compositions. An "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, 30 or substantially free of chemical precursors or other chemicals when chemically synthesized. Preferably, an "isolated" nucleic acid is free of sequences (preferably protein encoding sequences) that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic

DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention or biologically active portion thereof is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein-of-interest chemicals.

Fragments and variants of the disclosed nucleotide sequences and proteins encoded thereby are also encompassed by the present invention. By "fragment" is intended a portion of the nucleotide sequence or a portion of the amino acid sequence and hence protein encoded thereby. Fragments of a nucleotide sequence may encode protein fragments that retain the biological activity of the native protein and hence their altered expression enhances resistance to pathogens. Alternatively, fragments of a nucleotide sequence that are useful as hybridization probes generally do not encode protein fragments retaining biological activity. Thus, fragments of a nucleotide sequence may range from at least about 20 nucleotides, about 50 nucleotides, about 100 nucleotides, and up to the full-length nucleotide sequence encoding the proteins of the invention.

A fragment of a *Mlo* nucleotide sequence that encodes a biologically active portion of a *Mlo* protein of the invention will encode at least 15, 20, 25, 30, 40, 50, 75, 100, 200, 250, 300, 350, 400, 450, 500, or 550 contiguous amino acids, or up to the total number of amino acids present in a full-length MLO protein of the invention. (For example, 509, 499, and 492, amino acids for SEQ ID NOS: 6, 12, and 14 respectively.) Fragments of a *Mlo* nucleotide sequence that are useful as hybridization probes for PCR primers generally need not encode a biologically active portion of a MLO protein.

Thus, a fragment of a *Mlo* nucleotide sequence may encode a biologically active portion of a MLO protein, or it may be a fragment that can be used as a hybridization probe or PCR primer using methods disclosed below.



A biologically active portion of a MLO protein can be prepared by isolating a portion of one of the *Mlo* nucleotide sequences of the invention, expressing the encoded portion of the MLO protein (e.g., by recombinant expression *in vitro*), and assessing the activity of the encoded portion of the MLO protein. Nucleic acid molecules that are fragments of a *Mlo* nucleotide sequence comprise at least 16, 20, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 800, 900, 1,000, 1,100, 1,200, 1,300, 1,400, 1,500, 1,600, 1,700, 1,800, 1,900, and 2,000 nucleotides, or up to the number of nucleotides present in a full-length *Mlo* nucleotide sequence disclosed herein.

By "variants" is intended substantially similar sequences. For nucleotide sequences, conservative variants include those sequences that, because of the degeneracy of the genetic code, encode the amino acid sequence of one of the MLO polypeptides of the invention. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques as outlined below. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those generated, for example, by using site-directed mutagenesis but which still encode a MLO protein of the invention. Generally, nucleotide sequence variants of the invention will have at least 40%, 50%, 60%, 70%, generally, 80%, preferably 85%, 90%, up to 95%, 98% sequence identity to its respective native nucleotide sequence.

By "variant" protein is intended a protein derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may result from, for example, genetic polymorphism or from human manipulation.

The proteins of the invention may be altered in various ways including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the *Mlo* proteins can be prepared by mutations in the DNA.

Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel (1985) *Proc. Natl. Acad. Sci. USA* 82:488-492; Kunkel *et al.* (1987) *Methods in Enzymol.* 154:367-382; US Patent No. 4,873,192; Walker and Gaastra, eds. (1983) *Techniques in Molecular Biology* (MacMillan Publishing Company, New York) and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff *et al.* (1978) *Atlas of Protein Sequence and Structure* (Natl. Biomed. Res. Found., Washington, D.C.), herein incorporated by reference. Conservative substitutions, such as exchanging one amino acid with another having similar properties, may be preferred.

Thus, the genes and nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant forms. Likewise, the proteins of the invention encompass both naturally occurring proteins as well as variations and modified forms thereof. Such variants will continue to possess the desired ability to enhance resistance to pathogens when their expression is altered. Obviously, the mutations that will be made in the DNA encoding the variant must not place the sequence out of reading frame and preferably will not create complementary regions that could produce secondary mRNA structure. See, EP Patent Application Publication No. 75,444.

The deletions, insertions, and substitutions of the protein sequences encompassed herein are not expected to produce radical changes in the characteristics of the protein. However, when it is difficult to predict the exact effect of the substitution, deletion, or insertion in advance of doing so, one skilled in the art will appreciate that the effect will be evaluated by routine screening assays. That is, the activity can be evaluated by an enhanced resistance to pathogens when the expression of the protein sequences is altered.

Variant nucleotide sequences and proteins also encompass sequences and proteins derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different *Mlo* coding sequences can be manipulated to create a new *Mlo* coding sequence possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising

sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. For example, using this approach, sequence motifs encoding a domain of interest may be shuffled between the *Mlo* gene of the invention and other known genes involved in pathogen resistance to  
5 obtain a new gene coding for a protein with an improved property of interest, such as an increased  $K_m$  in the case of an enzyme. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751; Stemmer (1994) *Nature* 370:389-391; Cramer *et al.* (1997) *Nature Biotech.* 15:436-438; Moore *et al.* (1997) *J. Mol. Biol.*  
10 272:336-347; Zhang *et al.* (1997) *Proc. Natl. Acad. Sci. USA* 94:4504-4509; Cramer *et al.* (1998) *Nature* 391:288-291; and U.S. Patent Nos. 5,605,793 and 5,837,458.

The maize *Mlo* homologues are associated with disease related loci as shown in Table 3. Mapping information of the sequences are given in Table 5.  
15 The maize homologue proteins are predicted to be membrane-anchored by at least six, and possibly seven membrane-spanning helices. The maize sequences find use in negative control function of the MLO protein in leaf cell death and in the onset of pathogen defense. Generally, the methods of the invention take advantage of the absence of MLO to prime responsiveness of the plant to  
20 disease.

The nucleotide sequences of the invention can be used to isolate corresponding sequences from other organisms, particularly other plants, more particularly other monocots. In this manner, methods such as PCR, hybridization, and the like can be used to identify such sequences based on their  
25 sequence homology to the sequences set forth herein. Sequences isolated based on their sequence identity to the entire *Mlo* sequences set forth herein or to fragments thereof are encompassed by the present invention.

In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or  
30 genomic DNA extracted from any plant of interest. Methods for designing PCR primers and PCR cloning are generally known in the art and are disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York). See also Innis *et al.*,

eds. (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, New York); Innis and Gelfand, eds. (1995) *PCR Strategies* (Academic Press, New York); and Innis and Gelfand, eds. (1999) *PCR Methods Manual* (Academic Press, New York). Known methods of PCR include, but are not  
5 limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially-mismatched primers, and the like.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide  
10 sequences present in a population of cloned genomic DNA fragments or cDNA fragments (*i.e.*, genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as <sup>32</sup>P, or any other detectable marker. Thus, for example, probes  
15 for hybridization can be made by labeling synthetic oligonucleotides based on the *Mlo* sequences of the invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press,  
20 Plainview, New York).

For example, the entire sequence of the *Mlo* nucleotide sequences disclosed herein, or one or more portions thereof, may be used as a probe capable of specifically hybridizing to corresponding *Mlo* sequences and messenger RNAs. To achieve specific hybridization under a variety of  
25 conditions, such probes include sequences that are unique among *Mlo* sequences and are preferably at least about 10 nucleotides in length, and most preferably at least about 20 nucleotides in length. Such probes may be used to amplify corresponding *Mlo* sequences from a chosen plant by PCR. This technique may be used to isolate additional coding sequences from a desired  
30 plant or as a diagnostic assay to determine the presence of coding sequences in a plant. Hybridization techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, for example, Sambrook *et al.*

(1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

Hybridization of such sequences may be carried out under stringent conditions. By "stringent conditions" or "stringent hybridization conditions" is intended conditions under which a probe will hybridize to its target sequence to a detectably greater degree than to other sequences (e.g., at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences that are 100% complementary to the probe can be identified (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, preferably less than 500 nucleotides in length.

Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C.

Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the  $T_m$  can be approximated from the equation of Meinkoth and Wahl (1984) *Anal. Biochem.* 138:267-284:  $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$ ; where M is the

molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe.  $T_m$  is reduced by about 1°C for each 1% of mismatching; thus,  $T_m$ , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with  $\geq 90\%$  identity are sought, the  $T_m$  can be decreased 10°C. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point ( $T_m$ ); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point ( $T_m$ ); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point ( $T_m$ ). Using the equation, hybridization and wash compositions, and desired  $T_m$ , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a  $T_m$  of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 (Elsevier, New York); and Ausubel *et al.*, eds. (1995) *Current Protocols in Molecular Biology*, Chapter 2 (Greene Publishing and Wiley-Interscience, New York). See Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

In general, sequences that encode for a Mlo protein and hybridize to the Mlo sequences disclosed herein will be at least 40% to 50% homologous, about 60% to 70% homologous, and even about 80%, 85%, 90%, 95% to 98% homologous or more with the disclosed sequences. That is, the sequence

similarity of sequences may range, sharing at least about 40% to 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to 98% sequence similarity.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence",  
5 (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length  
10 cDNA or gene sequence, or the complete cDNA or gene sequence.

(b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not  
15 comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically  
20 introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith *et al.* (1981) *Adv. Appl. Math.* 2:482; by the homology alignment algorithm of Needleman *et al.* (1970) *J. Mol. Biol.*  
25 48:443; by the search for similarity method of Pearson *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:2444; by computerized implementations of these algorithms, including, but not limited to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View, California; GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer  
30 Group (GCG), 575 Science Drive, Madison, Wisconsin, USA; the CLUSTAL program is well described by Higgins *et al.* (1988) *Gene* 73:237-244 (1988); Higgins *et al.* (1989) *CABIOS* 5:151-153; Corpet *et al.* (1988) *Nucleic Acids Res.* 16:10881-90; Huang *et al.* (1992) *Computer Applications in the*

*Biosciences* 8:155-65, and Person *et al.* (1994) *Meth. Mol. Biol.* 24:307-331; preferred computer alignment methods also include the BLASTP, BLASTN, and BLASTX algorithms (see Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410). Alignment is also often performed by inspection and manual alignment.

5           (c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences makes reference to the residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not  
10 identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct  
15 for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity". Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity.  
20 Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

25           (d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or  
30 deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total



number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%  
5 sequence identity, preferably at least 80%, more preferably at least 90%, and most preferably at least 95%, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by  
10 taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 60%, more preferably at least 70%, 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical  
15 is if two molecules hybridize to each other under stringent conditions. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C, depending upon the desired degree of stringency as  
20 otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially  
25 identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70% sequence  
30 identity to a reference sequence, preferably 80%, more preferably 85%, most preferably at least 90% or 95% sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman *et al.* (1970) *J. Mol.*

*Biol.* 48:443. An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution. Peptides that are "substantially similar" share sequences as noted above except that residue positions that are not identical may differ by conservative amino acid changes.

The invention is drawn to methods for creating or enhancing resistance in a plant to plant pests by modulating the activity of *Mlo* genes in the plant. While the invention is not bound by any particular mechanism of action, it is believed that the methods of the invention will result in broad-based resistance in the modified plant. Accordingly, the methods are also useful in protecting plants against fungal pathogens, viruses, nematodes, insects and the like.

By "modulating activity" is intended that the expression of the *Mlo* gene is altered in some manner. Such modulation (increase or decrease) of expression results in enhanced resistance to pathogens. Generally, the methods of the invention will result in a decrease in the native protein or in protein activity. Thus, plants and plant cells are obtained having altered levels of MLO protein, preferably a decrease in protein levels. Such plants, plant cells and plant tissues are "modified" in that MLO protein levels are altered. As noted below, various methods are available for creating modified plants, plant cells and plant tissues including transformation and transfection leading to altered *Mlo* expression in the modified plant, plant cell or tissue.

The invention is drawn to compositions and methods for inducing resistance in a plant to plant pests. Accordingly, the compositions and methods are also useful in protecting plants against fungal pathogens, viruses, nematodes, insects and the like.

By "disease resistance" is intended that the plants avoid the disease symptoms that are the outcome of plant-pathogen interactions. That is, pathogens are prevented from causing plant diseases and the associated disease symptoms, or alternatively, the disease symptoms caused by the pathogen is minimized or lessened. The methods of the invention can be utilized to protect

plants from disease, particularly those diseases that are caused by plant pathogens.

Pathogens of the invention include, but are not limited to, viruses or viroids, bacteria, insects, nematodes, fungi, and the like. Viruses include any plant virus, for example, tobacco or cucumber mosaic virus, ringspot virus, necrosis virus, maize dwarf mosaic virus, etc. Specific fungal and viral pathogens for the major crops include: Soybeans: *Phytophthora megasperma* fsp. *glycinea*, *Macrophomina phaseolina*, *Rhizoctonia solani*, *Sclerotinia sclerotiorum*, *Fusarium oxysporum*, *Diaporthe phaseolorum* var. *sojae* (10) (*Phomopsis sojae*), *Diaporthe phaseolorum* var. *caulivora*, *Sclerotium rolfsii*, *Cercospora kikuchii*, *Cercospora sojina*, *Peronospora manshurica*, *Colletotrichum dematium* (*Colletotrichum truncatum*), *Corynespora cassiicola*, *Septoria glycines*, *Phyllosticta sojicola*, *Alternaria alternata*, *Pseudomonas syringae* p.v. *glycinea*, *Xanthomonas campestris* p.v. *phaseoli*, *Microsphaera* (15) *diffusa*, *Fusarium semitectum*, *Phialophora gregata*, Soybean mosaic virus, *Glomerella glycines*, Tobacco Ring spot virus, Tobacco Streak virus, *Phakopsora pachyrhizi*, *Pythium aphanidermatum*, *Pythium ultimum*, *Pythium debaryanum*, Tomato spotted wilt virus, *Heterodera glycines* *Fusarium solani*; Canola: *Albugo candida*, *Alternaria brassicae*, *Leptosphaeria maculans*, (20) *Rhizoctonia solani*, *Sclerotinia sclerotiorum*, *Mycosphaerella brassicicola*, *Pythium ultimum*, *Peronospora parasitica*, *Fusarium roseum*, *Alternaria alternata*; Alfalfa: *Clavibacter michiganense* subsp. *insidiosum*, *Pythium ultimum*, *Pythium irregulare*, *Pythium splendens*, *Pythium debaryanum*, *Pythium aphanidermatum*, *Phytophthora megasperma*, *Peronospora* (25) *trifoliorum*, *Phoma medicaginis* var. *medicaginis*, *Cercospora medicaginis*, *Pseudopeziza medicaginis*, *Leptotrochila medicaginis*, *Fusarium*, *Xanthomonas campestris* p.v. *alfalfae*, *Aphanomyces euteiches*, *Stemphylium herbarum*, *Stemphylium alfalfae*; Wheat: *Pseudomonas syringae* p.v. *atrofaciens*, *Urocystis agropyri*, *Xanthomonas campestris* p.v. *translucens*, *Pseudomonas* (30) *syringae* p.v. *syringae*, *Alternaria alternata*, *Cladosporium herbarum*, *Fusarium graminearum*, *Fusarium avenaceum*, *Fusarium culmorum*, *Ustilago tritici*, *Ascochyta tritici*, *Cephalosporium gramineum*, *Colletotrichum graminicola*, *Erysiphe graminis* f.sp. *tritici*, *Puccinia graminis* f.sp. *tritici*,

- Puccinia recondita* f.sp. *tritici*, *Puccinia striiformis*, *Pyrenophora tritici-repentis*, *Septoria nodorum*, *Septoria tritici*, *Septoria avenae*,  
*Pseudocercospora herpotrichoides*, *Rhizoctonia solani*, *Rhizoctonia cerealis*,  
*Gaeumannomyces graminis* var. *tritici*, *Pythium aphanidermatum*, *Pythium*  
5 *arrhenomanes*, *Pythium ultimum*, *Bipolaris sorokiniana*, Barley Yellow Dwarf  
Virus, Brome Mosaic Virus, Soil Borne Wheat Mosaic Virus, Wheat Streak  
Mosaic Virus, Wheat Spindle Streak Virus, American Wheat Striate Virus,  
*Claviceps purpurea*, *Tilletia tritici*, *Tilletia laevis*, *Ustilago tritici*, *Tilletia*  
*indica*, *Rhizoctonia solani*, *Pythium arrhenomannes*, *Pythium graminicola*,  
10 *Pythium aphanidermatum*, High Plains Virus, European wheat striate virus;  
Sunflower: *Plasmophora halstedii*, *Sclerotinia sclerotiorum*, Aster Yellows,  
*Septoria helianthi*, *Phomopsis helianthi*, *Alternaria helianthi*, *Alternaria*  
*zinniae*, *Botrytis cinerea*, *Phoma macdonaldii*, *Macrophomina phaseolina*,  
*Erysiphe cichoracearum*, *Rhizopus oryzae*, *Rhizopus arrhizus*, *Rhizopus*  
15 *stolonifer*, *Puccinia helianthi*, *Verticillium dahliae*, *Erwinia carotovorum* pv.  
*carotovora*, *Cephalosporium acremonium*, *Phytophthora cryptogea*, *Albugo*  
*tragopogonis*; Corn: *Fusarium moniliforme* var. *subglutinans*, *Erwinia*  
*stewartii*, *Fusarium moniliforme*, *Gibberella zeae* (*Fusarium graminearum*),  
*Stenocarpella maydi* (*Diplodia maydis*), *Pythium irregulare*, *Pythium*  
20 *debaryanum*, *Pythium graminicola*, *Pythium splendens*, *Pythium ultimum*,  
*Pythium aphanidermatum*, *Aspergillus flavus*, *Bipolaris maydis* O, T  
(*Cochliobolus heterostrophus*), *Helminthosporium carbonum* I, II & III  
(*Cochliobolus carbonum*), *Exserohilum turcicum* I, II & III, *Helminthosporium*  
*pedicellatum*, *Physoderma maydis*, *Phyllosticta maydis*, *Kabatiella-maydis*,  
25 *Cercospora sorghi*, *Ustilago maydis*, *Puccinia sorghi*, *Puccinia polysora*,  
*Macrophomina phaseolina*, *Penicillium oxalicum*, *Nigrospora oryzae*,  
*Cladosporium herbarum*, *Curvularia lunata*, *Curvularia inaequalis*, *Curvularia*  
*pallescentis*, *Clavibacter michiganense* subsp. *nebraskense*, *Trichoderma viride*,  
Maize Dwarf Mosaic Virus A & B, Wheat Streak Mosaic Virus, Maize  
30 Chlorotic Dwarf Virus, *Claviceps sorghi*, *Pseudonomas avenae*, *Erwinia*  
*chrysanthemi* pv. *zea*, *Erwinia carotovora*, Corn stunt *spiroplasma*, *Diplodia*  
*macrospora*, *Sclerophthora macrospora*, *Peronosclerospora sorghi*,  
*Peronosclerospora philippinensis*, *Peronosclerospora maydis*,

- Peronosclerospora sacchari*, *Sphacelotheca reiliana*, *Physopella zae*,  
*Cephalosporium maydis*, *Cephalosporium acremonium*, Maize Chlorotic Mottle  
 Virus, High Plains Virus, Maize Mosaic Virus, Maize Rayado Fino Virus,  
 Maize Streak Virus, Maize Stripe Virus, Maize Rough Dwarf Virus; Sorghum:  
 5 *Exserohilum turcicum*, *Colletotrichum graminicola* (*Glomerella graminicola*),  
*Cercospora sorghi*, *Gloeocercospora sorghi*, *Ascochyta sorghina*,  
*Pseudomonas syringae* p.v. *syringae*, *Xanthomonas campestris* p.v. *holcicola*,  
*Pseudomonas andropogonis*, *Puccinia purpurea*, *Macrophomina phaseolina*,  
*Perconia circinata*, *Fusarium moniliforme*, *Alternaria alternata*, *Bipolaris*  
 10 *sorghicola*, *Helminthosporium sorghicola*, *Curvularia lunata*, *Phoma insidiosa*,  
*Pseudomonas avenae* (*Pseudomonas alboprecipitans*), *Ramulispora sorghi*,  
*Ramulispora sorghicola*, *Phyllachara sacchari*, *Sporisorium reilianum*  
 (*Sphacelotheca reiliana*), *Sphacelotheca cruenta*, *Sporisorium sorghi*,  
 Sugarcane mosaic H, Maize Dwarf Mosaic Virus A & B, *Claviceps sorghi*,  
 15 *Rhizoctonia solani*, *Acremonium strictum*, *Sclerophthora macrospora*,  
*Peronosclerospora sorghi*, *Peronosclerospora philippinensis*, *Sclerospora*  
*graminicola*, *Fusarium graminearum*, *Fusarium oxysporum*, *Pythium*  
*arrhenomanes*, *Pythium graminicola*, etc.

- Nematodes include parasitic nematodes such as root-knot, cyst, lesion,  
 20 and reniform nematodes, etc.

- Insect pests include insects selected from the orders Coleoptera, Diptera,  
 Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthoptera,  
 Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera, Trichoptera, etc.,  
 particularly Coleoptera and Lepidoptera. Insect pests of the invention for the  
 25 major crops include: Maize: *Ostrinia nubilalis*, European corn borer; *Agrotis*  
*ipsilon*, black cutworm; *Helicoverpa zea*, corn earworm; *Spodoptera*  
*frugiperda*, fall armyworm; *Diatraea grandiosella*, southwestern corn borer;  
*Elasmopalpus lignosellus*, lesser cornstalk borer; *Diatraea saccharalis*,  
 sugarcane borer; *Diabrotica virgifera*, western corn rootworm; *Diabrotica*  
 30 *longicornis barberi*, northern corn rootworm; *Diabrotica undecimpunctata*  
*howardi*, southern corn rootworm; *Melanotus* spp., wireworms; *Cyclocephala*  
*borealis*, northern masked chafer (white grub); *Cyclocephala immaculata*,  
 southern masked chafer (white grub); *Popillia japonica*, Japanese beetle;

- Chaetocnema pulicaria*, corn flea beetle; *Sphenophorus maidis*, maize billbug; *Rhopalosiphum maidis*, corn leaf aphid; *Anuraphis maidiradicis*, corn root aphid; *Blissus leucopterus leucopterus*, chinch bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus sanguinipes*, migratory grasshopper;
- 5 *Hylemya platura*, seedcorn maggot; *Agromyza parvicornis*, corn blot leafminer; *Anaphothrips obscurus*, grass thrips; *Solenopsis milesta*, thief ant; *Tetranychus urticae*, twospotted spider mite; Sorghum: *Chilo partellus*, sorghum borer; *Spodoptera frugiperda*, fall armyworm; *Helicoverpa zea*, corn earworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Feltia subterranea*, granulate
- 10 cutworm; *Phyllophaga crinita*, white grub; *Eleodes*, *Conoderus*, and *Aeolus* spp., wireworms; *Oulema melanopus*, cereal leaf beetle; *Chaetocnema pulicaria*, corn flea beetle; *Sphenophorus maidis*, maize billbug; *Rhopalosiphum maidis*, corn leaf aphid; *Sipha flava*, yellow sugarcane aphid; *Blissus leucopterus leucopterus*, chinch bug; *Contarinia sorghicola*, sorghum
- 15 midge; *Tetranychus cinnabarinus*, carmine spider mite; *Tetranychus urticae*, twospotted spider mite; Wheat: *Pseudaletia unipunctata*, army worm; *Spodoptera frugiperda*, fall armyworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Agrotis orthogonia*, western cutworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Oulema melanopus*, cereal leaf beetle;
- 20 *Hypera punctata*, clover leaf weevil; *Diabrotica undecimpunctata howardi*, southern corn rootworm; Russian wheat aphid; *Schizaphis graminum*, greenbug; *Macrosiphum avenae*, English grain aphid; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Melanoplus sanguinipes*, migratory grasshopper; *Mayetiola destructor*, Hessian
- 25 fly; *Sitodiplosis mosellana*, wheat midge; *Meromyza americana*, wheat stem maggot; *Hylemya coarctata*, wheat bulb fly; *Frankliniella fusca*, tobacco thrips; *Cephus cinctus*, wheat stem sawfly; *Aceria tulipae*, wheat curl mite; Sunflower: *Suleima helianthana*, sunflower bud moth; *Homoeosoma electellum*, sunflower
- 30 beetle; *zygogramma exclamationis*, sunflower beetle; *Bothyrus gibbosus*, carrot beetle; *Neolasioptera murtfeldtiana*, sunflower seed midge; Cotton: *Heliothis virescens*, cotton budworm; *Helicoverpa zea*, cotton bollworm; *Spodoptera exigua*, beet armyworm; *Pectinophora gossypiella*, pink bollworm; *Anthonomus grandis grandis*, boll weevil; *Aphis gossypii*, cotton aphid; *Pseudatomoscelis*

*seriatus*, cotton fleahopper; *Trialeurodes abutilonea*, bandedwinged whitefly;  
*Lygus lineolaris*, tarnished plant bug; *Melanoplus femurrubrum*, redlegged  
 grasshopper; *Melanoplus differentialis*, differential grasshopper; *Thrips tabaci*,  
 onion thrips; *Frankliniella fusca*, tobacco thrips; *Tetranychus cinnabarinus*,  
 5 carmine spider mite; *Tetranychus urticae*, twospotted spider mite; Rice:  
*Diatraea saccharalis*, sugarcane borer; *Spodoptera frugiperda*, fall armyworm;  
*Helicoverpa zea*, corn earworm; *Colaspis brunnea*, grape colaspis;  
*Lissorhoptrus oryzophilus*, rice water weevil; *Sitophilus oryzae*, rice weevil;  
*Nephotettix nigropictus*, rice leafhopper; *Blissus leucopterus leucopterus*,  
 10 chinch bug; *Acrosternum hilare*, green stink bug; Soybean: *Pseudoplusia*  
*includens*, soybean looper; *Anticarsia gemmatilis*, velvetbean caterpillar;  
*Plathypena scabra*, green cloverworm; *Ostrinia nubilalis*, European corn borer;  
*Agrotis ipsilon*, black cutworm; *Spodoptera exigua*, beet armyworm; *Heliothis*  
*virescens*, cotton budworm; *Helicoverpa zea*, cotton bollworm; *Epilachna*  
 15 *varivestis*, Mexican bean beetle; *Myzus persicae*, green peach aphid; *Empoasca*  
*fabae*, potato leafhopper; *Acrosternum hilare*, green stink bug; *Melanoplus*  
*femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential  
 grasshopper; *Hylemya platura*, seedcorn maggot; *Sericothrips variabilis*,  
 soybean thrips; *Thrips tabaci*, onion thrips; *Tetranychus turkestani*, strawberry  
 20 spider mite; *Tetranychus urticae*, twospotted spider mite; Barley: *Ostrinia*  
*nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Schizaphis*  
*graminum*, greenbug; *Blissus leucopterus leucopterus*, chinch bug; *Acrosternum*  
*hilare*, green stink bug; *Euschistus servus*, brown stink bug; *Delia platura*,  
 seedcorn maggot; *Mayetiola destructor*, Hessian fly; *Petrobia latens*, brown  
 25 wheat mite; Oil Seed Rape: *Brevicoryne brassicae*, cabbage aphid; *Phyllotreta*  
*cruciferae*, Flea beetle; *Mamestra configurata*, Bertha armyworm; *Plutella*  
*xylostella*, Diamond-back moth; *Delia* ssp., Root maggots.

The present invention exploits the use of *Mlo* genes. The *Mlo* sequences  
 provided herein can be utilized to alter the expression of native *Mlo* genes in  
 30 plants. The *mlo* mutation confers recessive resistance to pathogens. Broad  
 spectrum resistance in plants can be enhanced by defective *Mlo* genes.

While the invention is not bound by any model, *Mlo* could have a  
 negative control function in leaf cell death. In this model, *Mlo* would suppress a

default cell suicide program in foliar tissue. Also, the MLO protein could have a specific negative regulatory function which works by down-regulating multiple disease-related functions. In this instance, spontaneous cell death in *mlo* mutant genotypes merely represents cell death because of accumulating  
5 activation of defense responses.

Several methods are available in the art for modulating the activity of *Mlo* genes. *Mlo* antisense sequences can be expressed in the plant cell. Such sequences will function to decrease expression of the maize *Mlo* genes as well as *Mlo* genes in other plants where the *Mlo* sequences share sequence identity.

10 It is recognized that with these nucleotide sequences, antisense constructions, complementary to at least a portion of the messenger RNA (mRNA) for the *Mlo* sequences can be constructed. Antisense nucleotides are constructed to hybridize with the corresponding mRNA. Modifications of the antisense sequences may be made as long as the sequences hybridize to and  
15 interfere with expression of the corresponding mRNA. In this manner, antisense constructions having 70%, preferably 80%, more preferably 85% sequence similarity to the corresponding antisensed sequences may be used. Furthermore, portions of the antisense nucleotides may be used to disrupt the expression of the target gene. Generally, sequences of at least 50 nucleotides,  
20 100 nucleotides, 200 nucleotides, or greater may be used.

The antisense construct may be proximal to the 5'-terminus or capping site, downstream from the capping site, between the capping site and the initiation codon and may cover all or a portion of the non-coding region. Additionally, the sequence may bridge the non-coding and coding region, be  
25 complementary to all or part of the coding region, to the 3'-terminus of the coding region, or complementary to the 3'-untranslated region of the mRNA.

It is recognized that the particular site to which the antisense sequence binds and the length of the antisense sequence will vary depending upon the degree of inhibition desired, the uniqueness of the sequence, the stability of the  
30 antisense sequence, and the like. See, for example, U.S. Patent Nos. 5,453,566; 5,530,192; and 5,728,926; all of which are herein incorporated by reference.

The nucleotide sequences of the present invention may also be used in the sense orientation to suppress the expression of endogenous genes in plants.



Methods for suppressing gene expression in plants using nucleotide sequences in the sense orientation are known in the art. The methods generally involve transforming plants with a DNA construct comprising a promoter that drives expression in a plant operably linked to at least a portion of a nucleotide  
5 sequence that corresponds to the transcript of the endogenous gene. Typically, such a nucleotide sequence has substantial sequence identity to the sequence of the transcript of the endogenous gene, preferably greater than about 65% sequence identity, more preferably greater than about 85% sequence identity, most preferably greater than about 95% sequence identity. See, U.S. Patent  
10 Nos. 5,283,184 and 5,034,323; herein incorporated by reference.

Individual *Mlo* genes or sets of *Mlo* genes can be rendered nonfunctional by mutagenesis. Such mutagenesis techniques include transposon disruption and recovery of such disruptions by reverse genetics approaches. Likewise, transformation-mediated mutagenesis may be utilized.

15 Disruption may be accomplished by transformation with gene replacement or gene truncation-disruption. See, for example, Bowen *et al.* (1995) *Mol. Gen. Gent.* 246:196-205; Walz *et al.* (1993) *Curr. Gent.* 25:421-427; Sweigard *et al.* (1992) *Mol. Gen. Gent.* 232:183-190; Hohn and Desjardins (1992) *Mol. Plant Microbe Interact* 5:249-256; Weber and Laitner (1994) *Curr.*  
20 *Gent.* 26:461-467; Templeton *et al.* (1994) *Gene* 142:141-146; Grolach *et al.* (1998) *Appl. Environ. Microbiol.* 64:385-391; Schaeffer *et al.* (1994) *Appl. Environ. Microbiol.* 60:594-598; and the like, herein incorporated by reference. See also, Kempin *et al.* (1997) *Nature* 389:802-803 and Koncz *et al.* (1992) *Plant Mol. Biol.* 20:963-976.

25 Alternatively, the naturally occurring *Mlo* sequence or sequences may be modified by site-directed mutagenesis. Such methods may be utilized to induce specific alterations in targeted genes. One means for site-directed mutagenesis includes targeting modification or mutation of the *Mlo* sequences by homologous recombination. The method involves the use of RNA-DNA  
30 hybrid oligonucleotides. Such nucleotides exploit the natural recombinogenicity of RNA-DNA hybrids. The oligonucleotides are duplex oligonucleotides that share homology with at least one *Mlo* sequence. While any region of the *Mlo* sequence can be targeted, it may be preferable to target

the 5' region of the *Mlo* sequence. See, for example, U.S. Patent No. 5,565,350 that describes chimeric oligonucleotides useful for targeted gene correction for use in cultured mammalian cells; as well as U.S. provisional application Serial No. 06/065,628 drawn to gene manipulation in plant cells, herein incorporated  
5 by reference. Such methods can be used to alter or disrupt the ATG start codon for the gene.

Alternatively, protein coding regions of *Mlo* genes can be altered in such a manner that the gene products or proteins perform their function in a dominant negative manner resulting in a resistant phenotype. See, for example Krylov *et al.* (1997) *Proc. Natl. Acad. Sci. USA* 94:12274-12279.  
10

Where the method of the invention relies upon the expression of an altered *Mlo* sequence or an *Mlo* antisense sequence in a plant, a number of promoters can be used. The promoters can be selected from constitutive and/or inducible promoters. Such promoters include those from pathogenesis-related  
15 proteins (PR proteins), which are induced following infection by a pathogen; e.g., PR proteins, SAR proteins, beta-1,3-glucanase, chitinase, etc. See, for example, Redolfi *et al.* (1983) *Neth. J. Plant Pathol.* 89:245-254; Uknes *et al.* (1992) *The Plant Cell* 4:645-656; and Van Loon (1985) *Plant Mol. Virol.* 4:111-116. See, also copending application entitled "Inducible Maize promoters",  
20 filed and herein incorporated by reference.

Of interest are promoters that are expressed locally at or near the site of pathogen infection. See, for example, Marineau *et al.* (1987) *Plant Mol. Biol.* 9:335-342; Matton *et al.* (1989) *Molecular Plant-Microbe Interactions* 2:325-331; Somsisch *et al.* (1986) *Proc. Natl. Acad. Sci. USA* 83:2427-2430;  
25 Somsisch *et al.* (1988) *Molecular and General Genetics* 2:93-98; and Yang, Y (1996) *Proc. Natl. Acad. Sci. USA* 93:14972-14977. See also, Chen *et al.* (1996) *Plant J.* 10:955-966; Zhang and Sing (1994) *Proc. Natl. Acad. Sci. USA* 91:2507-2511; Warner *et al.* (1993) *Plant J.* 3:191-201; Siebertz *et al.* (1989) *Plant Cell* 1:961-968; and the references cited therein. Of particular interest is  
30 the inducible promoter for the maize PRms gene, whose expression is induced by the pathogen *Fusarium moniliforme* (see, for example, Cordero *et al.* (1992) *Physiological and Molecular Plant Pathology* 41:189-200).

Constitutive promoters include, for example, the core promoter of the Rsyn7 (copending application serial number 08/661,601), the 35S promoter, the core 35S promoter, and the like. Other constitutive promoters include, for example, U.S. Patent Nos. 5,608,149; 5,608,144; 5,604,121; 5,569,597; 5,466,785; 5,399,680; 5,268,463; 5,608,142. See also, copending application  
5 entitled "Constitutive Maize Promoters" Provisional Application Serial No. 60/076,075 filed February 26, 1998, and herein incorporated by reference.

Tissue specific promoters include Yamamoto *et al.* (1997) *Plant J.* 12(2):255-265; Kawamata *et al.* (1997) *Plant Cell Physiol.* 38(7):792-803;  
10 Hansen *et al.* (1997) *Mol. Gen Genet.* 254(3):337-343; Russell *et al.* (1997) *Transgenic Res.* 6(2):157-168; Rinehart *et al.* (1996) *Plant Physiol.* 112(3):1331-1341; Van Camp *et al.* (1996) *Plant Physiol.* 112(2):525-535; Canevascini *et al.* (1996) *Plant Physiol.* 112(2):513-524; Yamamoto *et al.* (1994) *Plant Cell Physiol.* 35(5):773-778; Lam (1994) *Results Probl. Cell.*  
15 *Differ.* 20:181-196; Orozco *et al.* (1993) *Plant Mol. Biol.* 23(6):1129-1138; Matsuoka *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90(20):9586-9590; and Guevara-Garcia *et al.* (1993) *Plant J.* 4(3):495-505.

The methods of the invention can be used with other methods for increasing pathogen resistance in plants. See, for example, Cai *et al.* (1997)  
20 *Science* 275:832-834; Roberts and Galloway (1984) *J. Heredity* 75:147-148; Ryerson and Heath (1996) *Plant Cell* 8:393-402 and Dangl *et al.* (1996) *Plant Cell* 8:1793-1807.

Altered *Mlo* sequences or antisense *Mlo* sequences of the invention can be introduced into any plant. The sequences to be introduced may be used in  
25 expression cassettes for expression in any plant of interest where expression in the plant cell is necessary. In other instances, such as for recombination, oligonucleotides are synthesized, purified and introduced into the plant cell.

Where expression cassettes are needed, such expression cassettes will comprise a transcriptional initiation region linked to the coding sequence or  
30 antisense sequence of the nucleotide of interest. Such an expression cassette is provided with a plurality of restriction sites for insertion of the sequence to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes.

The transcriptional initiation region, the promoter, may be native or analogous or foreign or heterologous to the plant host. Additionally, the promoter may be the natural sequence or alternatively a synthetic sequence. By foreign is intended that the transcriptional initiation region is not found in the native plant into which the transcriptional initiation region is introduced. As used herein a chimeric gene comprises a coding sequence operably linked to a transcription initiation region that is heterologous to the coding sequence.

While it may be preferable to express the sequences using heterologous promoters, the native promoter sequences may be used. Such constructs would change expression levels of a MLO protein in the plant or plant cell. Thus, the phenotype of the plant or plant cell is altered.

The transcriptional cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also, Guerineau *et al.* (1991) *Mol. Gen. Genet.* 262:141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon *et al.* (1991) *Genes Dev.* 5:141-149; Mogen *et al.* (1990) *Plant Cell.* 2:1261-1272; Munroe *et al.* (1990) *Gene* 91:151-158; Ballas *et al.* (1989) *Nucleic Acids Res.* 17:7891-7903; Joshi *et al.* (1987) *Nucleic Acid Res.* 15:9627-9639.

Nucleotide sequences of the invention are provided in expression cassettes for expression in the plant of interest. The cassette will include 5' and 3' regulatory sequences operably linked to the sequence of interest. The cassette may additionally contain at least one additional sequence to be cotransformed into the organism. Alternatively, the additional sequence(s) can be provided on another expression cassette.

Where appropriate, the gene(s) may be optimized for increased expression in the transformed plant. That is, the genes can be synthesized using plant-preferred codons for improved expression. See, for example, Campbell

and Gowri (1990) *Plant Physiol.* 92:1-11 for a discussion of host-preferred codon usage. Methods are available in the art for synthesizing plant-preferred genes. See, for example, U.S. Patent Nos. 5,380,831, 5,436,391, and Murray *et al.* (1989) *Nucleic Acids Res.* 17:477-498, herein incorporated by reference.

5 Additional sequence modifications are known to enhance gene expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation signals, exon-intron splice site signals, transposon-like repeats, and other such well-characterized sequences that may be deleterious to gene expression. The G-C content of the sequence may be adjusted to levels  
10 average for a given cellular host, as calculated by reference to known genes expressed in the host cell. When possible, the sequence is modified to avoid predicted hairpin secondary mRNA structures.

The expression cassettes may additionally contain 5' leader sequences in the expression cassette construct. Such leader sequences can act to enhance  
15 translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein *et al.* (1989) *PNAS USA* 86:6126-6130); potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison *et al.* (1986); MDMV leader (Maize Dwarf Mosaic Virus); *Virology* 154:9-20), and human  
20 immunoglobulin heavy-chain binding protein (BiP), (Macejak *et al.* (1991) *Nature* 353:90-94); untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4) (Jobling *et al.* (1987) *Nature* 325:622-625); tobacco mosaic virus leader (TMV) (Gallie *et al.* (1989) in *Molecular Biology of RNA*, ed. Cech (Liss, New York), pp. 237-256); and maize chlorotic mottle  
25 virus leader (MCMV) (Lommel *et al.* (1991) *Virology* 81:382-385). See also, Della-Cioppa *et al.* (1987) *Plant Physiol.* 84:965-968. Other methods known to enhance translation can also be utilized, for example, introns, and the like.

In preparing the expression cassette, the various DNA fragments may be manipulated, so as to provide for the DNA sequences in the proper orientation  
30 and, as appropriate, in the proper reading frame. Towards this end, adapters or linkers may be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites, removal of superfluous DNA, removal of restriction sites, or the like. For this purpose, *in*

*vitro* mutagenesis, primer repair, restriction, annealing, resubstitutions, e.g. transitions and transversions, may be involved.

The sequences of the present invention can be used to transform or transfect any plant. In this manner, genetically modified plants, plant cells, plant tissue, seed, and the like can be obtained. Transformation protocols as well as protocols for introducing nucleotide sequences into plants may vary depending on the type of plant or plant cell, i.e., monocot or dicot, targeted for transformation. Suitable methods of introducing nucleotide sequences into plant cells and subsequent insertion into the plant genome include microinjection (Crossway *et al.* (1986) *Biotechniques* 4:320-334), electroporation (Riggs *et al.* (1986) *Proc. Natl. Acad. Sci. USA* 83:5602-5606, *Agrobacterium*-mediated transformation (Townsend *et al.*, U.S. Pat No. 5,563,055), direct gene transfer (Paszkowski *et al.* (1984) *EMBO J.* 3:2717-2722), and ballistic particle acceleration (see, for example, Sanford *et al.*, U.S. Patent No. 4,945,050; Tomes *et al.* (1995) "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment," in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg and Phillips (Springer-Verlag, Berlin); and McCabe *et al.* (1988) *Biotechnology* 6:923-926). Also see Weissinger *et al.* (1988) *Ann. Rev. Genet.* 22:421-477; Sanford *et al.* (1987) *Particulate Science and Technology* 5:27-37 (onion); Christou *et al.* (1988) *Plant Physiol.* 87:671-674 (soybean); McCabe *et al.* (1988) *Bio/Technology* 6:923-926 (soybean); Finer and McMullen (1991) *In Vitro Cell Dev. Biol.* 27P:175-182 (soybean); Singh *et al.* (1998) *Theor. Appl. Genet.* 96:319-324 (soybean); Datta *et al.* (1990) *Biotechnology* 8:736-740 (rice); Klein *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:4305-4309 (maize); Klein *et al.* (1988) *Biotechnology* 6:559-563 (maize); Tomes, U.S. Patent No. 5,240,855; Buising *et al.*, U.S. Patent Nos. 5,322,783 and 5,324,646; Tomes *et al.* (1995) "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment," in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg (Springer-Verlag, Berlin) (maize); Klein *et al.* (1988) *Plant Physiol.* 91:440-444 (maize); Fromm *et al.* (1990) *Biotechnology* 8:833-839 (maize); Hooykaas-Van Slogteren *et al.* (1984) *Nature (London)* 311:763-764; Bowen *et al.*, U.S. Patent No. 5,736,369 (cereals); Bytebier *et al.* (1987) *Proc. Natl. Acad. Sci. USA*

84:5345-5349 (Liliaceae); De Wet *et al.* (1985) in *The Experimental Manipulation of Ovule Tissues*, ed. Chapman *et al.* (Longman, New York), pp. 197-209 (pollen); Kaeppler *et al.* (1990) *Plant Cell Reports* 9:415-418 and Kaeppler *et al.* (1992) *Theor. Appl. Genet.* 84:560-566 (whisker-mediated transformation); D'Halluin *et al.* (1992) *Plant Cell* 4:1495-1505 (electroporation); Li *et al.* (1993) *Plant Cell Reports* 12:250-255 and Christou and Ford (1995) *Annals of Botany* 75:407-413 (rice); Osjoda *et al.* (1996) *Nature Biotechnology* 14:745-750 (maize via *Agrobacterium tumefaciens*); all of which are herein incorporated by reference.

10       The modified plant may be grown into plants in accordance with conventional ways. See, for example, McCormick *et al.* (1986) *Plant Cell Reports*, 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having the desired phenotypic characteristic identified. Two or more generations may  
15 be grown to ensure that the subject phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure the desired phenotype or other property has been achieved.

      The *Mlo* sequences of the invention are also useful as molecular markers. Such markers are useful in breeding programs, particularly those  
20 aimed at improving disease resistance. The maize *Mlo* sequences have been mapped to chromosome locations and these positions related to known disease resistance loci.

      The present invention provides a method of genotyping a plant comprising a polynucleotide of the present invention. Preferably, the plant is a  
25 monocot, such as maize or sorghum. Genotyping provides a means of distinguishing homologs of a chromosome pair and can be used to differentiate segregants in a plant population. Molecular marker methods can be used for phylogenetic studies, characterizing genetic relationships among crop varieties, identifying crosses or somatic hybrids, localizing chromosomal segments  
30 affecting monogenic traits, map based cloning, and the study of quantitative inheritance. See, e.g., *Plant Molecular Biology: A Laboratory Manual*, Chapter 7, Clark, Ed., Springer-Verlag, Berlin (1997). For molecular marker methods, see generally, *The DNA Revolution* by Andrew H. Paterson (1996)

(Chapter 2) in: Genome Mapping in Plants (ed. Andrew H. Paterson) by Academic Press/R. G. Landis Company, Austin, Texas, pp. 7-21.

The particular method of genotyping in the present invention may employ any number of molecular marker analytic techniques such as, but not  
5 limited to, restriction fragment length polymorphisms (RFLPs). RFLPs are the product of allelic differences between DNA restriction fragments caused by nucleotide sequence variability. As is well known to those of skill in the art, RFLPs are typically detected by extraction of genomic DNA and digestion with a restriction enzyme. Generally, the resulting fragments are separated according  
10 to size and hybridized with a probe; single copy probes are preferred. Restriction fragments from homologous chromosomes are revealed. Differences in fragment size among alleles represent an RFLP. Thus, the present invention further provides a means to follow segregation of a gene or nucleic acid of the present invention as well as chromosomal sequences  
15 genetically linked to these genes or nucleic acids using such techniques as RFLP analysis. Linked chromosomal sequences are within 50 centiMorgans (Cm), often within 40 or 30 Cm, preferably within 20 or 10 Cm, more preferably within 5, 3, 2, or 1 Cm of a gene.

In the present invention, the nucleic acid probes employed for molecular  
20 marker mapping of plant nuclear genomes selectively hybridize, under selective hybridization conditions, to a gene encoding a polynucleotide of the present invention. In preferred embodiments, the probes are selected from polynucleotides of the present invention. Typically, these probes are cDNA probes or *PstI* genomic clones. The length of the probes is discussed in greater  
25 detail, *supra*, but are typically at least 15 bases in length, more preferably at least 20, 25, 30, 35, 40, or 50 bases in length. Generally, however, the probes are less than about 1 kilobase in length. Preferably, the probes are single copy probes that hybridize to a unique locus in a haploid chromosome complement. Some exemplary restriction enzymes employed in RFLP mapping are EcoRI,  
30 EcoRV, and SstI. As used herein the term "restriction enzyme" includes reference to a composition that recognizes and, alone or in conjunction with another composition, cleaves at a specific nucleotide sequence.



The method of detecting an RFLP comprises the steps of (a) digesting genomic DNA of a plant with a restriction enzyme; (b) hybridizing a nucleic acid probe, under selective hybridization conditions, to a sequence of a polynucleotide of the present of said genomic DNA; (c) detecting therefrom a RFLP. Other methods of differentiating polymorphic (allelic) variants of polynucleotides of the present invention can be had by utilizing molecular marker techniques well known to those of skill in the art including such techniques as: 1) single-stranded conformation analysis (SSCP); 2) denaturing gradient gel electrophoresis (DGGE); 3) Rnase protection assays; 4) allele-specific oligonucleotides (ASOs); 5) the use of proteins which recognize nucleotide mismatches, such as the *E. coli* mutS protein; and 6) allele-specific PCR. Other approaches based on the detection of mismatches between the two complementary DNA strands include clamped denaturing gel electrophoresis (CDGE); heteroduplex analysis (HA); and chemical mismatch cleavage (CMC). Exemplary polymorphic variants are provided in Table I, *supra*. Thus, the present invention further provides a method of genotyping comprising the steps of contacting, under stringent hybridization conditions, a sample suspected of comprising a polynucleotide of the present invention with a nucleic acid probe. Generally, the sample is a plant sample; preferably, a sample suspected of comprising a maize polynucleotide of the present invention (e.g., gene, mRNA). The nucleic acid probe selectively hybridizes, under stringent conditions, to a subsequence of a polynucleotide of the present invention comprising a polymorphic marker. Selective hybridization of the nucleic acid probe to the polymorphic marker nucleic acid sequence yields a hybridization complex. Detection of the hybridization complex indicates the presence of that polymorphic marker in the sample. In preferred embodiments, the nucleic acid probe comprises a polynucleotide of the present invention.

The following examples are offered by way of illustration and not by way of limitation.

## EXPERIMENTAL

### Mlo Sequences

Eight maize *Mlo* homologue sequences have been identified. The nucleotide sequences (SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, and 15) and amino acid sequences (SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, and 16) are provided. DNA sequence analysis was performed according to Sambrook *et al.* (1989) *Mol. Cloning: A Laboratory Manual*, 2nd ed. (Cold Spring Harbor Laboratory Press, Plainview, New York). The maize *Mlo* homologue/orthologue cDNA sequences were identified from mRNA isolated from various maize tissues and used to make cDNAs that are then cloned into vectors, usually pSPORT1. These cDNA libraries are EST sequenced via standard dye-fluorescence labeling and ABI machine electrophoresis and image capture. The *Mlo* homologues were identified by their blast score identity to the barley HvMLO1 published sequence. These maize clones, in particular the longest members of each contig or gene, were obtained and additional sequencing was done on them using oligonucleotide primers designed to internal portions of the cDNA and dye-fluorescence labeling and ABI machine electrophoresis and image capture. The complete edited sequences were assembled and analyzed.

The sequences from maize show sequence similarity to the published barley *Mlo* sequence as provided in Tables 1 and 2. Figure 1 provides a sequence alignment for the maize *Mlo* homologues with the barley *Mlo* sequence designated as HvMlo1. Figure 2 groups the *Mlo* sequences based on relatedness as well as the plant tissue from which it was isolated.

The ZmMLO genes were mapped by RFLP analysis using Southern blots of genomic DNA isolated from F2 and F3 and F4 segregating maize populations. The DNA was isolated using a modified CTAB adapted from the CERES RFLP Lab Manuel based on the Saghai-Mahoof procedure (Saghai-Mahoof *et al.* (1984) *Proc. Natl. Acad. Sci. USA* 81:8014-8018). Genomic DNA was cut with four restriction enzymes *Bam*HI, *Eco*RI, *Eco*RV, and *Hind*III and run (5µg/lane) on 0.8% TAE agarose gels for 800 volt-hours. The gels were Southern blot transferred to Hybond-N membrane (Amersham Life Science), baked and UV-crosslinked. The ZmMLO cDNA inserts were liberated from its vector by cleaving with two restriction enzymes, usually *Sal*I

and *NotI*, and the insert was purified from agarose gels following electrophoresis. The clone was random prime labeled with  $^{32}\text{P}$ -dCTP using the RTS (Gibco BRL) labeling kit. The cDNA inserts were used to probe parental screening blots to identify a mapping population with a RFLP polymorphism.

- 5 Once a polymorphism was identified, the inserts were used to probe mapping blots containing DNA from segregating individuals. The map position was determined using MAPMAKER/EXP 3.0 (Lander *et al* (1987) *Genomics* 1:174-181) by scoring 86 segregating progeny as homozygous parent A, as
- 10 homozygous parent B, or as heterozygous. The map position was assigned to an existing core RFLP map of either of the following three populations: ALEB9 (240 individuals) DRAG2 (283 individuals) or MARS (1075 individuals).

Table 3 shows the association of maize *Mlo* homologues and disease related loci and QTLS.

TABLE I

BestFit (Similarity/Identity)

Maize MLO Gene	HvMLO1	ZmMLO1	ZmMLO2	ZmMLO4	ZmMLO5	ZmMLO6	ZmMLO7	ZmMLO8	ZmMLO9
HvMLO1	100%	67	53	35	45	58	40	44	37
ZmMLO1	72	100%	45	35	38	51	39	43	39
ZmMLO2	61	56	100%	40	48	58	43	46	40
ZmMLO4	47	44	49	100%	46	38	39	40	46
ZmMLO5	54	47	56	56	100%	45	50	76	41
ZmMLO6	66	61	66	48	51	100%	41	43	39
ZmMLO7	48	49	52	48	58	52	100%	56	41
ZmMLO8	54	55	56	52	81	54	64	100%	43
ZmMLO9	48	48	49	51	56	50	51	56	100%

Protein (Similarity/Identity) to:

TABLE 2

Gap (Similarity/Identity)		Protein Homology (Similarity/Identity) to:								
Maize <i>MLO</i> Gene	Hv <i>MLO1</i>	Zm <i>MLO1</i>	Zm <i>MLO2</i>	Zm <i>MLO4</i>	Zm <i>MLO5</i>	Zm <i>MLO6</i>	Zm <i>MLO7</i>	Zm <i>MLO8</i>	Zm <i>MLO9</i>	
Hv <i>MLO1</i>	100%	66	43	31	33	55	36	40	32	
Zm <i>MLO1</i>	71	100%	36	24	32	43	28	37	28	
Zm <i>MLO2</i>	53	46	100%	36	36	57	39	45	34	
Zm <i>MLO4</i>	42	31	46	100%	32	34	35	37	42	
Zm <i>MLO5</i>	40	38	42	38	100%	43	42	60	36	
Zm <i>MLO6</i>	63	51	64	43	49	100%	40	41	36	
Zm <i>MLO7</i>	43	35	47	43	48	51	100%	51	40	
Zm <i>MLO8</i>	49	48	54	49	67	52	59	100%	40	
Zm <i>MLO9</i>	40	36	42	53	48	46	44	51	100%	

TABLE 3  
Association of Maize *MLO* Homologues and Disease Related Loci and QTLs

<u>Maize <i>MLO</i> Homologue</u>	<u>Nearby Disease Resistance Loci or QTLs</u>
ZmMLO1 1.01	1.01 European Corn Borer QTL
	1.01/2 Northern Corn Leaf Blight QTL
ZmMLO2 1.04	1.03/6 Northern Corn Leaf Blight QTL
	1.04 Gray Leaf Spot QTL
	1.04 Maize Streak Virus ( <i>msvl</i> )
	1.05 Stewart's Wilt QTL
ZmMLO4 3.05	3.04/5 European Corn Borer QTL
	3.04/5 Gibberella Stalk Rot QTL
ZmMLO5 3.06	3.07/8 Northern Corn Leaf Blight QTL
ZmMLO6a 5.05	5.04 Gibberella Stalk Rot QTL
	5.06 Northern Corn Leaf Blight QTL
ZmMLO6b 6.02/3	6.01 Southern Corn Leaf Blight ( <i>rhml</i> )
ZmMLO7 6.05/7	
ZmMLO8 9.04	9.05 Southwestern Corn Borer QTL
ZmMLO9 na	

TABLE 4

Mutator Insertion Mutants of *ZmMLO* Homologues (TUSC)

5	<i>ZmMLO2</i>	
	PV03 81D3	<i>C. heterostrophus</i> intermediate resistance (segregating as recessive)
10	PV03 81D2 (sib)	<i>C. heterostrophus</i> intermediate resistance (segregating as recessive)
	PV03 108B1	<i>C. heterostrophus</i> intermediate resistance (segregating as recessive)
	PV03 108A1 (sib)	<i>C. heterostrophus</i> resistance (segregating as recessive)
15	BT94 5F11	<i>C. heterostrophus</i> resistance (segregating as recessive); also leaf necrosis

The Trait Utility System for corn (TUSC) system was utilized to generate transposon mutants in the *Mlo* sequences in maize. The combination of transposon mutagenesis via *Mutator* and PCR-based selection of target-specific *Mu* insertions makes up the TUSC system. See, for example, Benson *et al.* (1995) *Plant Cell*. 7:75-84; Mena *et al.* (1996) *Science* 274:1537-1540; U.S. Patent Application No. 08/835,638 and U.S. Patent Application No. 08/262,056; all of which are herein incorporated by reference. Table 4 shows *Mutator* insertion mutants of *ZmMlo* homologues.

Oligonucleotide primers based on *Mlo* maize sequences were designed and paired with *Mu* TIR primer in PCR reactions. The products of the screening process identify individuals in the collection having *Mu* elements inserted into *Mlo* sequences.

The gene-specific primers used for TUSC of *ZmMLO2* are: 19005, 5'-AGTTATCCAAGGCATGCCGGTGGTAAACT-3' (SEQ ID NO:18); and 19007, 5'-AAGTCATCGAGGGAGGCATCACTTACAG-3' (SEQ ID NO:19). For TUSC the mutator-element specific primer used was: 9242, 5'-AGAGAAGCCAACGCCA(AT)CGCCTC(CT)ATTTCGTC-3' (SEQ ID NO:20). Seven positive "hits" to *ZmMLO2* were identified. Twenty F2 seeds for each of the hits were planted in the greenhouse and screened as follows. Seeds were planted in trays, containing 2-inch wells for each seed, in Strong-Lite (circleR) Universal Mix potting soil (Universal Mix, Pine Bluff, Arkansas, U.S.A.) and grown in a greenhouse (16 hour day, 20.6-34.8°C, 50% average RH, 560-620 microEinsteins, of light both sun and halogen lamps, averaging 25 heat units per day. Plants were grown for 14-18 days until the V5 stage (ca. 25cm height) and inoculated with spores of *Cochliobolus heterostrophus* (Drechs.) Drechs. Race 0, also known as *Bipolaris maydis* (Southern Leaf Blight) and *Cochliobolus carbonum* R. R Nelson, also known as *Bipolaris zeicola* (Helminthosporium Leaf Spot). For general leaf inoculation, spore suspensions of  $4 \times 10^4$  per ml of 0.02% Tween-20 were sprayed as an aerosol on the leaves. Approximately 0.5 ml were applied per leaf late in the afternoon. The plants were then immediately covered with a plastic tent and kept at R.T. in order to enhance humidity and spore germination. The plastic tent was removed early in the morning, and the plants were returned to the greenhouse for the duration of the experiment, usually three days. Susceptibility to *Cochliobolus carbonum* was determined by either increased size or number of lesions. Resistance to *Cochliobolus*



*heterostrophus* was determined by either reduced size or number of lesions. Lesion mimics were also investigated; these mutations form spontaneous lesions in the absence of pathogen attach. Other phenotypes affecting growth and development were also noted.

TABLE 5

Maize MLO Gene	ZmMLO1	ZmMLO2	ZmMLO4	ZmMLO5	ZmMLO6a	ZmMLO6b	ZmMLO7	ZmMLO8	ZmMLO9
Gene Mapping Information									
Gene Complexity on Southern blot	1	1	1	1	2	2	1	1, 2	1, 2
Chromosome location (bin)	1.01	1.04	3.05	3.06	5.05	6.02/3	9.04	6.05/7	unassigned
Chromosome location (arm)	1S	1S	3L	3L	5L	6L	9L	6L	
Nearby Public Marker	Bnl5.62	Bnl12.06	umc10	bnl10.24	umc43	umc113	umc95	bnl5.47	
Distance from Public Marker	12.3 (down)	10.1 (down)	6.5 (down)	1.3 (up)	10.9 (down)	52.0 (up)	6.3 (down)	10.1 (up)	
Distance	15	5.9	35.2	1.3	1.8	52	10.7	10.1	
LOD Score	18.2	24.1	21.3	31.7	35.2	4.6	36.5	23.8	
RFLP Restriction Enzyme	EcoRI	HindIII	EcoRV	EcoRI	BamHI	BamHI	HindIII	EcoRV	
Mapping Population	ALEB9	ALEB9	DRAG2	ALEB9	DRAG2	DRAG2	DRAG2	DRAG2	DRAG2
Mapping Parents (Public Names)	R67/P38	R67/P38	17J/MWO	R67/P38	17J/MWO	17J/MWO	17J/MWO	17J/MWO	17J/MWO

TABLE 6

Maize <i>MLO</i> Gene	HvMLO1	ZmMLO	ZmMLO2	ZmMLO4	ZmMLO5	ZmMLO6	ZmMLO7	ZmMLO8	ZmMLO9
Protein Structure Predictions									
Number of amino acids	533	224+	565	509	149+	515	499	492	469+
Calculated molecular weight	60,408		64,274	58,613		56,980	56,806	55,500	
Calculated pI	9.7		9.6	9.3		9.5	8.9	9.3	
Number of transmembrane domains	6 or 7		6 or 7	6 or 7		6 or 7	6 or 7	6 or 7	
Glycosylation sites? Asn-X-Ser/Thr	0	0	1	3	2	1	1	0	
Signal Peptide	No	No	No	No	No	No	No	No	No

### Example 1: Transformation and Regeneration of Transgenic Plants

Immature maize embryos from greenhouse donor plants are bombarded with a plasmid containing the *ZmMLO1* antisense sequence operably linked to the ubiquitin promoter (Figure 3). This plasmid also contains the selectable marker gene PAT (Wohlleben *et al.* (1988) *Gene* 70:25-37) that confers resistance to the herbicide Bialophos. Transformation is performed as follows. All media recipes are in the Appendix.

#### Preparation of Target Tissue

The ears are surface sterilized in 30% Chlorox bleach plus 0.5% Micro detergent for 20 minutes, and rinsed two times with sterile water. The immature embryos are excised and placed embryo axis side down (scutellum side up), 25 embryos per plate, on 560Y medium for 4 hours and then aligned within the 2.5-cm target zone in preparation for bombardment.

#### Preparation of DNA

A plasmid vector comprising the PAT selectable marker and the *ZmMl01* antisense sequence operably linked to a the ubiquitin is made and precipitated onto 1.1  $\mu\text{m}$  (average diameter) tungsten pellets using a  $\text{CaCl}_2$  precipitation procedure as follows:

- 100  $\mu\text{l}$  prepared tungsten particles in water
- 10  $\mu\text{l}$  (1  $\mu\text{g}$ ) DNA in TrisEDTA buffer (1  $\mu\text{g}$  total)
- 100  $\mu\text{l}$  2.5 M  $\text{CaCl}_2$
- 10  $\mu\text{l}$  0.1 M spermidine

Each reagent is added sequentially to the tungsten particle suspension, while maintained on the multitube vortexer. The final mixture is sonicated briefly and allowed to incubate under constant vortexing for 10 minutes. After the precipitation period, the tubes are centrifuged briefly, liquid removed, washed with 500 ml 100% ethanol, and centrifuged for 30 seconds. Again the liquid is removed, and 105  $\mu\text{l}$  100% ethanol is added to the final tungsten particle pellet. For particle gun bombardment, the

tungsten/DNA particles are briefly sonicated and 10 µl spotted onto the center of each macrocarrier and allowed to dry about 2 minutes before bombardment.

#### Particle Gun Treatment

- 5           The sample plates are bombarded at level #4 in particle gun #HE34-1 or #HE34-2. All samples receive a single shot at 650 PSI, with a total of ten aliquots taken from each tube of prepared particles/DNA.

#### Subsequent Treatment

- 10           Following bombardment, the embryos are kept on 560Y medium for 2 days, then transferred to 560R selection medium containing 3 mg/liter Bialaphos, and subcultured every 2 weeks. After approximately 10 weeks of selection, selection-resistant callus clones are transferred to 288J medium to initiate plant regeneration. Following somatic embryo maturation (2-4 weeks), well-developed somatic embryos are transferred to
- 15           medium for germination and transferred to the lighted culture room. Approximately 7-10 days later, developing plantlets are transferred to 272V hormone-free medium in tubes for 7-10 days until plantlets are well established. Plants are then transferred to inserts in flats (equivalent to 2.5" pot) containing potting soil and grown for 1 week in a growth chamber, subsequently grown an additional 1-2 weeks in the greenhouse, then transferred to classic
- 20           600 pots (1.6 gallon) and grown to maturity. Plants are monitored and scored for enhanced disease resistance as a result of antisense disruption of *ZmMlo1* function.

**APPENDIX****272 V**

Ingredient	Amount	Unit
D-I H <sub>2</sub> O	950.000	MI
MS Salts (GIBCO 11117-074)	4.300	G
Myo-Inositol	0.100	G
MS Vitamins Stock Solution ##	5.000	MI
Sucrose	40.000	G
Bacto-Agar @	6.000	G

**Directions:**

- 5 @ = Add after bringing up to volume

Dissolve ingredients in polished D-I H<sub>2</sub>O in sequence

Adjust to pH 5.6

Bring up to volume with polished D-I H<sub>2</sub>O after adjusting pH

Sterilize and cool to 60°C.

- 10 ## = Dissolve 0.100 g of Nicotinic Acid; 0.020 g of Thiamine.HCL; 0.100 g of Pyridoxine.HCL; and 0.400 g of Glycine in 875.00 ml of polished D-I H<sub>2</sub>O in sequence. Bring up to volume with polished D-I H<sub>2</sub>O. Make in 400 ml portions. Thiamine.HCL & Pyridoxine.HCL are in Dark Desiccator. Store for one month, unless contamination or precipitation occurs, then make fresh stock.
- 15 Total Volume (L) = 1.00

## 288 J

Ingredient	Amount	Unit
D-I H <sub>2</sub> O	950.000	ml
MS Salts	4.300	g
Myo-Inositol	0.100	g
MS Vitamins Stock Solution ##	5.000	ml
Zeatin .5mg/ml	1.000	ml
Sucrose	60.000	g
Gelrite @	3.000	g
Indoleacetic Acid 0.5 mg/ml #	2.000	ml
0.1mM Absciscic Acid	1.000	ml
Bialaphos 1mg/ml #	3.000	ml

## Directions:

@ = Add after bringing up to volume

- 5 Dissolve ingredients in polished D-I H<sub>2</sub>O in sequence

Adjust to pH 5.6

Bring up to volume with polished D-I H<sub>2</sub>O after adjusting pH

Sterilize and cool to 60°C.

Add 3.5g/L of Gelrite for cell biology.

- 10 ## = Dissolve 0.100 g of Nicotinic Acid; 0.020 g of Thiamine.HCL; 0.100 g of Pyridoxine.HCL; and 0.400 g of Glycine in 875.00 ml of polished D-I H<sub>2</sub>O in sequence. Bring up to volume with polished D-I H<sub>2</sub>O. Make in 400 ml portions. Thiamine.HCL & Pyridoxine.HCL are in Dark Desiccator. Store for one month, unless contamination or precipitation occurs, then make fresh stock.

- 15 Total Volume (L) = 1.00

## 560 R

Ingredient	Amount	Unit
D-I Water, Filtered	950.000	ml
CHU (N6) Basal Salts (SIGMA C-1416)	4.000	g
Eriksson's Vitamin Mix (1000X SIGMA-1511	1.000	ml
Thiamine.HCL 0.4mg/ml	1.250	ml
Sucrose	30.000	g
2, 4-D 0.5mg/ml	4.000	ml
Gelrite @	3.000	g
Silver Nitrate 2mg/ml #	0.425	ml
Bialaphos 1mg/ml #	3.000	ml

## Directions:

5 @ = Add after bringing up to volume

# = Add after sterilizing and cooling to temp.

Dissolve ingredients in D-I H<sub>2</sub>O in sequence

Adjust to pH 5.8 with KOH

Bring up to volume with D-I H<sub>2</sub>O

10 Sterilize and cool to room temp.

Total Volume (L) = 1.00



## 560 Y

Ingredient	Amount	Unit
D-I Water, Filtered	950.000	ml
CHU (N6) Basal Salts (SIGMA C-1416)	4.000	g
Eriksson's Vitamin Mix (1000X SIGMA-1511	1.000	ml
Thiamine.HCL 0.4mg/ml	1.250	ml
Sucrose	120.000	g
2,4-D 0.5mg/ml	2.000	ml
L-Proline	2.880	g
Gelrite @	2.000	g
Silver Nitrate 2mg/ml #	4.250	ml

## Directions:

@ = Add after bringing up to volume .

5 # = Add after sterilizing and cooling to temp.

Dissolve ingredients in D-I H<sub>2</sub>O in sequence

Adjust to pH 5.8 with KOH

Bring up to volume with D-I H<sub>2</sub>O

Sterilize and cool to room temp.

10 \*\* Autoclave less time because of increased sucrose\*\*

Total Volume (L) = 1.00


All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and  
5 individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims

INDICATIONS RELATING TO DEPOSITED MICROORGANISM  
OR OTHER BIOLOGICAL MATERIAL

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the deposited microorganism or other biological material referred to in the description on page 5, lines 11-20	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depository institution American Type Culture Collection	
Address of depository institution (including postal code and country) Manassa, Virginia USA	
Date of deposit	Accession Numbers 98725-98729
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indicators are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit") Date of Deposit	

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## WHAT IS CLAIMED IS:

1. A method for creating or enhancing disease resistance in a plant, said method comprising modulating the expression of an *Mlo* nucleotide sequence wherein said nucleotide sequence is selected from the group consisting of:

- (a) a nucleotide sequence encoding a maize *Mlo* gene;
- (b) a nucleotide sequence encoding at least one of the maize MLO amino acid sequences selected from the group consisting of the sequences set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, and 16;
- (c) a nucleotide sequence comprising at least one of the nucleotide sequences set forth in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, and 15;
- (d) a nucleotide sequence selected from the group consisting of sequences deposited in the American Type Culture Collection as Accession Nos. 98725, 98726, 98727, 98728, and 98729;
- (e) a nucleotide sequence that encodes an antisense sequence corresponding to a sequence of a), b), c) or d);
- (f) a nucleotide sequence which hybridizes under stringent conditions to one of the nucleotide sequences set forth in a), b), c), d) or e).

2. The method of claim 1, wherein said modulation comprises decreasing the expression of the *Mlo* sequence.

3. The method of claim 1, wherein said plant is a monocot.

4. The method of claim 3, wherein said monocot is maize.

5. A modified plant having altered levels of an MLO protein wherein said plant has stably incorporated into its genome a DNA construct, wherein said DNA construct comprises a nucleotide sequence operably linked

to a promoter capable of regulating transcription of said sequence in said plant, wherein said nucleotide sequence is selected from the group consisting of:

- (a) a nucleotide sequence encoding a maize *Mlo* gene;
- (b) a nucleotide sequence encoding at least one of the maize MLO amino acid sequences selected from the group consisting of the sequences set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, and 16;
- (c) a nucleotide sequence comprising at least one of the nucleotide sequences set forth in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, and 15;
- (d) a nucleotide sequence selected from the group consisting of sequences deposited in the American Type Culture Collection as Accession Nos. 98725, 98726, 98727, 98728, and 98729;
- (e) a nucleotide sequence that encodes an antisense sequence corresponding to a sequence of a), b), c) or d);
- (f) a nucleotide sequence which hybridizes under stringent conditions to one of the nucleotide sequences set forth in a), b), c), d) or e).

6. The modified plant of claim 5, wherein said plant exhibits a decrease in the expression of a *Mlo* gene.

7. The modified plant of claim 5, wherein said plant is a monocot.

8. The modified plant of claim 7, wherein said monocot is maize.

9. The maize plant of claim 8, wherein said plant has decreased levels of the *Mlo* protein.

10. The maize plant of claim 8, wherein said maize plant comprises an insertion sequence in at least one maize *Mlo* gene.

11. Seed of the plant of any one of claims 5, 6, 7, 8, 9, and 10.

12. An isolated MLO protein, wherein said protein comprises an amino acid sequence selected from the group consisting of the MLO amino acid sequences set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, and 16.

13. An isolated nucleotide sequence said sequence selected from the group consisting of:

- (a) a nucleotide sequence encoding a maize *Mlo* gene;
- (b) a nucleotide sequence encoding at least one of the maize MLO amino acid sequences selected from the group consisting of the sequences set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, and 16;
- (c) a nucleotide sequence comprising at least one of the nucleotide sequences set forth in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, and 15;
- (d) a nucleotide sequence selected from the group consisting of sequences deposited in the American Type Culture Collection as Accession Nos. 98725, 98726, 98727, 98728, and 98729;
- (e) a nucleotide sequence that encodes an antisense sequence corresponding to a sequence of a), b), c) or d);
- (f) a nucleotide sequence which hybridizes under stringent conditions to one of the nucleotide sequences set forth in a), b), c), d) or e).

14. A modified plant cell having an altered level of an MLO protein wherein said plant cell has stably incorporated into its genome a DNA construct, wherein said DNA construct comprises a nucleotide sequence operably linked to a promoter capable of regulating transcription of said sequence in said plant cell, wherein said nucleotide sequence is selected from the group consisting of:

- (a) a nucleotide sequence encoding a maize *Mlo* gene;
- (b) a nucleotide sequence encoding at least one of the maize MLO amino acid sequences selected from the group consisting of the sequences set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, and 16;
- (c) a nucleotide sequence comprising at least one of the nucleotide sequences set forth in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, and 15;

- (d) a nucleotide sequence selected from the group consisting of sequences deposited in the American Type Culture Collection as Accession Nos. 98725, 98726, 98727, 98728, and 98729;
- (e) a nucleotide sequence that encodes an antisense sequence corresponding to a sequence of a), b), c) or d);
- (f) a nucleotide sequence which hybridizes under stringent conditions to one of the nucleotide sequences set forth in a), b), c), d) or e).

15. The modified plant cell of claim 14, wherein said cell exhibits a decrease in the expression of an *Mlo* gene.

16. The modified plant cell of claim 14, wherein said cell is from a monocot.

17. The modified plant cell of claim 16, wherein said monocot is maize.

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## CLUSTAL W (1.7) Multiple Sequence Alignments of HvMLO1 and 9 ZmMLO Homologues

```

HvMLO1 -MSDKKGVPALELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEK
ZmMLO1 -----
ZmMLO2 MGGDG----TRALDQTPTWAVAACVAVIVAASILLEGFLHHLGQLLNKKRKKALFDALEK
ZmMLO6 MGGGGGGGNSRELDQTPTWAVASVCGVIVLISILLEKGLHHVGEFFSHRKKKAMVEALEK

ZmMLO7 -----MGKEATLAFPTWVVAIVCLVIVSISLAAERSLHYLGKYLECKKQKALFSALQR
ZmMLO5 -----
ZmMLO8 ---MAAEGEAALEFPTWIVAACSLIVLLSLVAERCLHYLGKTLKRKNQKPLFEALLK
ZmMLO9 -----
ZmMLO4 ---MAAEQGRSLAETPTWSVATVTTLMVAACFLVERSLSRFAKWLRKTKRKAMLALEK
Regions [---N-Terminus---] [---TM Helix 1---] [---Intervening Region 1---]

HvMLO1 MKAELMLVGFISLLLIVTQDPIIAKICISED-AADVMWPCKRGTEGRKPS-----
ZmMLO1 -----
ZmMLO2 VKSELMTLGFISLLLIVTGR-YIARICIPEG-AANTMLPCRLSGHSVAEEPKGHGRR---
ZmMLO6 VKAELMVLGFISLLLVFGQN-YIIKVCISNH-AANTMLPCKLEAAAVEGK-DGHGKEAAA

ZmMLO7 LKEELMLLGFISFVLSLSQG-FIVSICIPET-STDFMLPCNR-----GNS-----
ZmMLO5 -----
ZmMLO8 VKEELMLLGFISLLLVTFQG-MIRRTCIPER-WTFHMLPCEKPDEKAGEAATMEHFVGTL
ZmMLO9 -----
ZmMLO4 IREELMLLGVISLLLSQTAR-FISEICVPSSLFTRFYICSESDYQDLLRNTDANQTALD
---] [-----TM Helix 2-----] [-----Intervening Region 2-----]

HvMLO1 -----K-----YVDYCPEGKVA
ZmMLO1 -----
ZmMLO2 -----HLS-----EDPTNLFSCRKGMVS
ZmMLO6 VVAGKKKVAVAVPGKKKKKAAAAADHLGGVVDWPPPYAHNARMLAEASMAKCEPGKVP

ZmMLO7 -----RVAEEGAKICNKKGDVP
ZmMLO5 -----
ZmMLO8 GRIGRR-----LLQEGTAGAEQCQKKGKVP
ZmMLO9 -----HSPRRNLKTSYHNHEGCREGYES
ZmMLO4 -----KNMFGGQ-RLHVCGEHGP
-----Intervening Region 2-----

HvMLO1 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPAR-
ZmMLO1 -----
ZmMLO2 LVSADGMHQLHIFVFFLAVFHVTF SFF TMSLGRAKTRIWKVWEKETCSPQNYLNDPSK-
ZmMLO6 LISINALHQLHIFIFLAVFHVSYSAITMALGRAKIRAWKEWEKEAAGQDYEF SHDPTR-

ZmMLO7 LLSLEALHQLHIFIFVLGLVHVVF CATTISFSGAKMRKWKHWETEIHREVHEKLQQEKNE
ZmMLO5 -----
ZmMLO8 LLSLEAIHQLHIFIFVLAITHVIFS VTTMLLGGAIHQWKQWENGIKKDAPGNGPKVTN-
ZmMLO9 FVSHEGLEQLHRFIFVMVTHVTYSCLTMLLAILKIHKWRDWEDEAFRDNHESFSQIAYE
ZmMLO4 FVSYEGLEQLHRFLF ILGITHVLYSFVTVLSMIKITYSVRKWETLAGPIAEEEEKARRT-
-----] P-----TM Helix 3-----] [-----Intervening Region 3-----]

HvMLO1 -----FRFTHQTSFVKRHL--GLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGF
ZmMLO1 -----
ZmMLO2 -----FRLTHQTSFVRQHAS-CWSKSTITLYFVSFFRQFFRSVRKTDYF TLRHGF
ZmMLO6 -----FRFTHQTSFVRQHNM-VLNKFPASFYISNFFRQFFRSVRQADYCALRHSE

ZmMLO7 GQGSSLSIVVLHREHQDEFVHKRTKGFWMKLAVASWITAF LKQFQDSVSKSDYEALRSF
ZmMLO5 -----
ZmMLO8 -----VHHHEF IKRKFKGIGKDSIILSWLHSGKQFYRSVSKSDYTTMRLGF
ZmMLO9 S-----ATRRQPALTKSYSFRSVSQNNVVMWLVCFIAQFGQSVVRADYLILRKGF
ZmMLO4 -----KVMRRQSTFVFNNASHPWSKNKILIWMLCFLRQFKGSIIRSDYLALRLGF
-----Intervening Region 3-----

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TO FIG. 1B.

**FIG. 1A.**



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FROM FIG. 1A.

HvMLO1 INAHL SQNSKFDHFKYIKRSMEDDFKVVVGISLPLWGVAILTFLDINGVGTLIWISFIP  
ZmMLO1  
ZmMLO2 ISAHLS PGTRFNFRKYIKRSLEDDFKTVVGISPLWASALAVMLFNHVGWHLNFWFSAIP  
ZmMLO6 VNVHLAPGSKFDHFKYIDRSLEDDFKVIVGISPLWASALIFLFLNVNGWHTMLWISIMP  
ZmMLO7 VVEHYEKPDI DFHKYMTAVEYEFKRVVGISWYLWLFVILFLLNNGWHTYFWLAFLP  
ZmMLO5  
ZmMLO8 IMTHCPGNPKDFHRYMVRVLEADFKKVVGISWYLWVFVIFLLNNGWHTYFWIAFLP  
ZmMLO9 IMTHNLPPT-YDFHNYMIRSMEEFEKIVGVSGLLWGFVFAFMLFNVDGSNLYFWIAILP  
ZmMLO4 MTYHKLPHS-YDFHKYMVRSMEDDYNIGTIGISWPLWAYAIVCILNVHGINIYFWLSFVP  
---Intervening Region 3---] [---TM Helix 4---] [IR 4] [---TM  
HvMLO1 LVILLCVGKLEMIIMEMALEIQDRAS---VIKGAPVVEPSNKFVWHRPDWVLFHILTL  
ZmMLO1 ---EIQDKAT---VIKGAPVVEPSDRFFVFNRPQWVLFHILTL  
ZmMLO2 LVVILAVGKLAIIAMMAIEIAERHT---VIQGMPPVKLSDDHFWGKPRVLHLIHFAS  
ZmMLO6 VVILSVGKLGQIIICMAIDITERHA---VIQGI PMVQVSDSYFWARPTFVLFHIFTL  
ZmMLO7 LFLLLIVGAKLEGIITRLAQEAASLSN-NTEEVPKIKPCKDHFVWFKPELVHLIHFIL  
ZmMLO5 ---IHFIL  
ZmMLO8 LILLIAIGTKLEHVIAQLAHDVAEKHT---AVEGDVIVKPSDEHFWGKPRVILYL IHFIL  
ZmMLO9 VTLVLLVGAKLQHVIAITLTAEGAKMST---YGPRIQPRDDLFWFKKPEFLLWL IHFVIL  
ZmMLO4 VELVLLVGTQLQHVIAQLALEVAEATA---PY-VGSQLKL RDDLFVWFKPRVWLWL IGFIS  
Helix 5] [---Intervening Region 5---  
HvMLO1 FQNAFQMAHFVWTATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGS  
ZmMLO1 FQNAFQMAHFVWTLTPDLKKCYHERLGLSIMKVAVGLVLQVLCSYITFPLYALVTQMGS  
ZmMLO2 FQNAFEITYFFWIWYEFGLRSCFHDNFEFIARVCLGATVQFMCSYITLPLAYALVSQMGS  
ZmMLO6 FQNGFQIIYFLWILYEYGMDSFCNDSEEFV FARLCLGVVQVLC SYVTLPYALVSQMGS  
ZmMLO7 FQNSFEISFFFVILVSEGF GSCMMERKPYVISRLVIGVIEVECSYITLPLYAIVTHMTG  
ZmMLO5 FQNAFEIAFFFVILTTYGNSCIMDHVPFIVPRLVVGAIQLLCSYSTLPYAI VTQMG  
ZmMLO8 FQNAFEIAFFFVILSTYGF DSCIMGQVRFIVPRLVIGVVIQLLCSYSTLPYAI VTQMG  
ZmMLO9 GQNAFELASFFVFWQFGYDSCFIKNHLLVYCRLILGFAGQFLCSYSTLPYALVTQMGS  
ZmMLO4 FQNAFELATFLWLSVELSAQTCFMKHYMVAIRLISGLLVQFWCLYYSTLPNVIISQMGS  
---Intervening Region 4---] [---TM Helix6---] [---  
HvMLO1 NMKRSIFDEQTSKALTNWRNTAKEKKKVR---DTDLMAQMIGDAIPSRGSS-PMP SRGSS  
ZmMLO1 HMKRTIFEEQTAKAVMKWRKTAKDKVRQRE-AAGFLDVLTSADITPSHSRA-TSPSRGSS  
ZmMLO2 EMKRTIFDEQTAKALKKWKAVVKKKHHK-----DSSHNSSETPSTDTTGPAGEAGEV  
ZmMLO6 TMKDSIFDEQTSKALKNWRAGAKKKAPTG-----GSKHGGGGSPTAGGS-PTKADGDA  
ZmMLO7 QIKLHGF GSRVHESVHGWIGLRKKPFSFWKIPGGDPNADSGREADVTRRVAKERSGSSRS  
ZmMLO5 FFKKEIFDEHVQSSLLGWAQKAKKRKALRNNGNGSNGAAAG-SSHPSATARLELMRRAVA  
ZmMLO8 CYKKEIFNEHVQGGVLGWAQKVKMKKGLK--G-----AAS--ASKDESITNADSAGPSVK  
ZmMLO9 KYKAALIPRRIRETIHGWGKATRKRRRR--RGDDSTVRTETSTVCSLTDDEDFEDDD  
ZmMLO4 KFKKSLYSENVRESLHSWCKRVKDRSRHN--PLFSRNGLTTRSVCSLDTTYETDHEINT  
-----C-Terminus-----  
HvMLO1 -----PVHLLHKGM-----GRSDDPQSAPTSPRT-----QQEARDMPVVAH  
ZmMLO1 -----PVHLLHKYR-----GRSEEPQSGPASP-----GRELGDMPVADQH  
ZmMLO2 QRLHEVPVRHLHRYKTI-----AHVGGVRSPLSDPDYSDTDDTEPLSLQTRHLIPPAQR  
ZmMLO6 -----  
ZmMLO7 -----MPMAPADEI-----VTVDVAVAAAAVGGGP-----  
ZmMLO5 -----LEEGSAGGN-----GSEASAAELHDTGPKL-----  
ZmMLO8 -----IEMAKAG-----EDVEIVGNTG-----  
ZmMLO9 HHHHGPPSYDTPRAGGRPPYKIEITHRQSGSGHDGPRPGGTPCFHPSGSGSGHAMLLRQAS  
ZmMLO4 VCTLSRTASATSLDDQL-----TVVTVDDEPSCIEKDV-----  
-----C-Terminus-----

TO FIG. 1C.

FIG. 1B.

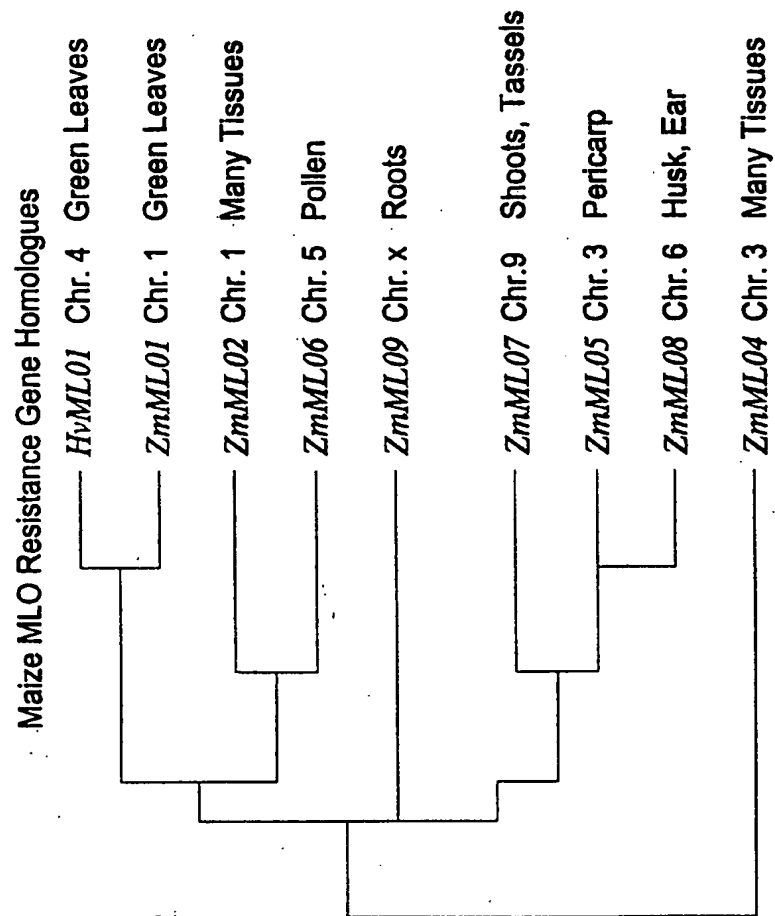
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FROM FIG. 1B.

HvMLO1	PVHRLNPNDRRRSASSSALEADIPSADFSFSQG-----	533	aa
ZmMLO1	RLHRLDP-ERM RPASSTAVNIDIADAFSFSMR-----	224	aa
ZmMLO2	SLDTERAEVRVNVVETAAAPSDVLQDSFSFPRLLPPRHVPDK--	565	aa
ZmMLO6	-----	515	aa
ZmMLO7	-----	499	aa
ZmMLO5	-----	149	aa
ZmMLO8	-----	492	aa
ZmMLO9	VSAPSSPSYRGGNNVTRSASMPGIAALRTTGSGTPTRVSHEEPT	469	aa
ZmMLO4	-----	509	aa
	-----C-Terminus-----		

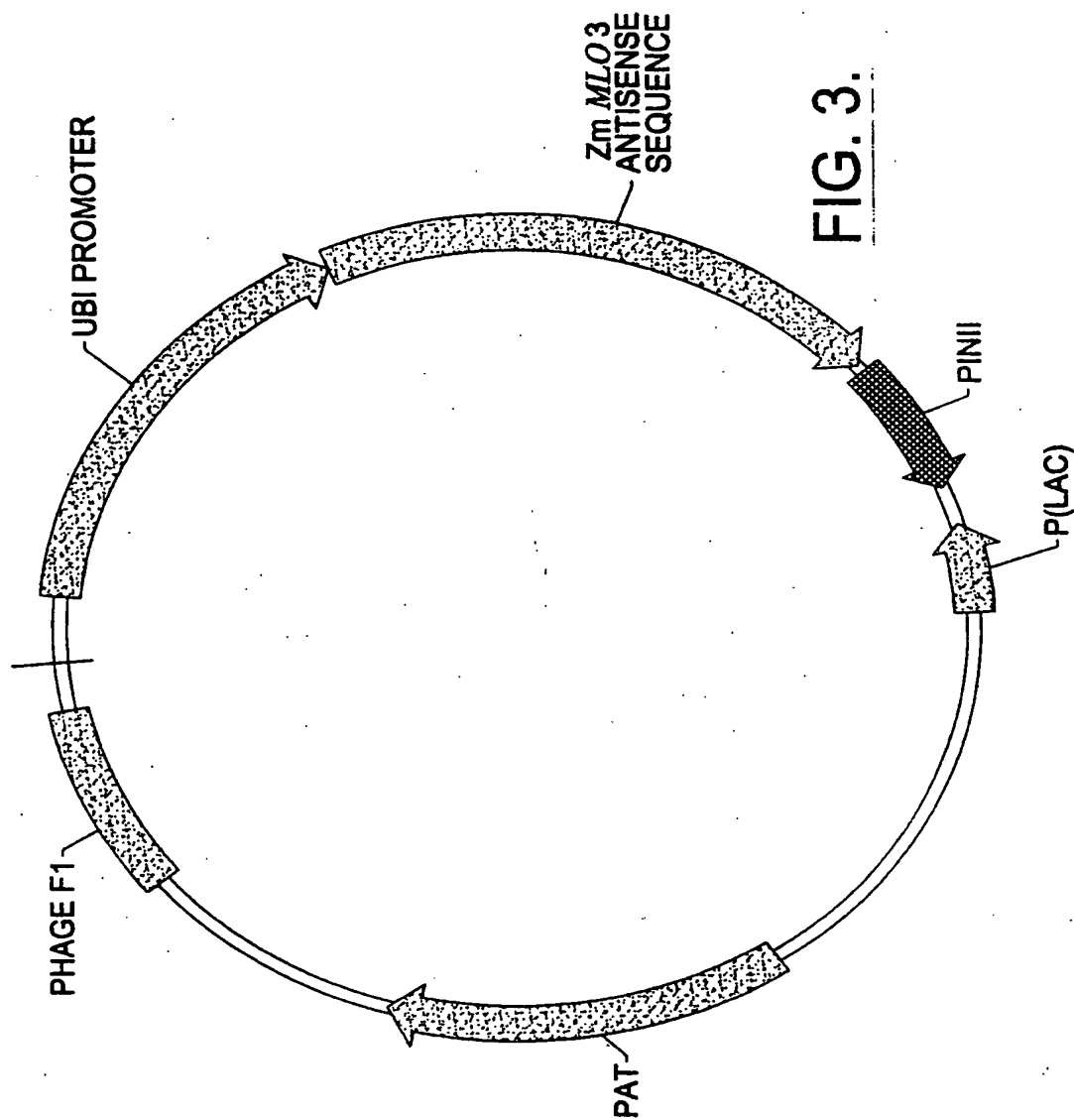
FIG. 1C.

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**FIG. 2.**

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## SEQUENCE LISTING

&lt;110&gt; Briggs, Steven

<120> Manipulation of Mlo Genes to Enhance Disease Resistance  
in Plants

&lt;130&gt; 5718-42035718/158714

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 20

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 845

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;223&gt; Ml01

&lt;400&gt; 1

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aggagataca ggacaaggcg acggtcatca agggggcgcc tgtggtggag ccaagtgaca 60
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agaacgcctt ccagatggcg catttcgttt ggacactgct caccacagac ctgaagaaat 180
gctaccacga gaggtgggct ctgagcatca tgaaagttgc ggtggggctg gttctccagg 240
tcctctgcag ctacatcacc ttcccgtctt acgcgtctgt cacgcagatg gggtcgcaca 300
tgaagaagac catcttcgag gagcagacgg ccaaggcggt gatgaagtgg cgcaagacgg 360
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aaaaa

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&lt;210&gt; 2

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;223&gt; Ml01

&lt;400&gt; 2

Glu Ile Gln Asp Lys Ala Thr Val Ile Lys Gly Ala Pro Val Val Glu  
 1 5 10 15

Pro Ser Asp Arg Phe Phe Trp Phe Asn Arg Pro Gly Trp Val Leu Phe  
 20 25 30

Leu Ile His Leu Thr Leu Phe Gln Asn Ala Phe Gln Met Ala His Phe  
 35 40 45

Val Trp Thr Leu Leu Thr Pro Asp Leu Lys Lys Cys Tyr His Glu Arg  
 50 55 60

Leu Gly Leu Ser Ile Met Lys Val Ala Val Gly Leu Val Leu Gln Val  
 65 70 75 80

Leu Cys Ser Tyr Ile Thr Phe Pro Leu Tyr Ala Leu Val Thr Gln Met  
 85 90 95

Gly Ser His Met Lys Lys Thr Ile Phe Glu Glu Gln Thr Ala Lys Ala  
 100 105 110

Val Met Lys Trp Arg Lys Thr Ala Lys Asp Lys Val Arg Gln Arg Glu  
 115 120 125

Ala Ala Gly Phe Leu Asp Val Leu Thr Ser Ala Asp Thr Thr Pro Ser  
 130 135 140

His Ser Arg Ala Thr Ser Pro Ser Arg Gly Asn Ser Pro Val His Leu  
 145 150 155 160

Leu His Lys Tyr Arg Gly Arg Ser Glu Glu Pro Gln Ser Gly Pro Ala  
 165 170 175

Ser Pro Gly Arg Glu Leu Gly Asp Met Tyr Pro Val Ala Asp Gln His  
 180 185 190

Arg Leu His Arg Leu Asp Pro Glu Arg Met Arg Pro Ala Ser Ser Thr  
 195 200 205

Ala Val Asn Ile Asp Ile Ala Asp Ala Asp Phe Ser Phe Ser Met Arg  
 210 215 220

<210> 3  
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 <213> Zea mays

<220>  
 <223> M1o2

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<210> 4  
 <211> 565  
 <212> PRT  
 <213> Zea mays

&lt;220&gt;

&lt;223&gt; M1o2

&lt;400&gt; 4

Met Gly Gly Asp Gly Thr Arg Ala Leu Asp Gln Thr Pro Thr Trp Ala  
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Val Ala Ala Val Cys Ala Val Ile Val Ala Ala Ser Ile Leu Leu Glu  
 20 25 30

Gly Phe Leu His His Leu Gly Gln Leu Leu Asn Lys Lys Arg Lys Lys  
 35 40 45

Ala Leu Phe Asp Ala Leu Glu Lys Val Lys Ser Glu Leu Met Thr Leu  
 50 55 60

Gly Phe Ile Ser Leu Leu Leu Thr Val Thr Gly Arg Tyr Ile Ala Arg  
 65 70 75 80

Ile Cys Ile Pro Glu Gly Ala Ala Asn Thr Met Leu Pro Cys Arg Leu  
 85 90 95

Ser Gly His Ser Val Ala Glu Glu Pro Lys Gly His Gly Arg Arg His  
 100 105 110

Leu Ser Glu Asp Pro Thr Asn Leu Phe Ser Cys Arg Lys Gly Met Val  
 115 120 125

Ser Leu Val Ser Ala Asp Gly Met His Gln Leu His Ile Phe Val Phe  
 130 135 140

Phe Leu Ala Val Phe His Val Thr Phe Ser Phe Phe Thr Met Ser Leu  
 145 150 155 160

Gly Arg Ala Lys Thr Arg Ile Trp Lys Val Trp Glu Lys Glu Thr Cys  
 165 170 175

Ser Pro Gln Tyr Asn Tyr Leu Asn Asp Pro Ser Lys Phe Arg Leu Thr  
 180 185 190

His Gln Thr Ser Phe Val Arg Gln His Ala Ser Cys Trp Ser Lys Ser  
 195 200 205

Thr Ile Thr Leu Tyr Phe Val Ser Phe Phe Arg Gln Phe Phe Arg Ser  
 210 215 220

Val Arg Lys Thr Asp Tyr Phe Thr Leu Arg His Gly Phe Ile Ser Ala



5

485

490

495

Asp Pro Asp Tyr Ser Asp Thr Asp Asp Thr Glu Pro Leu Ser Leu Gln  
500 505 510

Thr Arg His Leu Ile Pro Pro Ala Lys Gln Arg Ser Leu Asp Thr Glu  
515 520 525

Arg Ala Glu Val Arg Val Asn Val Val Glu Thr Ala Ala Ala Pro Ser  
530 535 540

Asp Val Leu Gln Asp Ser Phe Ser Phe Pro Arg Leu Leu Pro Pro Arg  
545 550 555 560

His Val Pro Asp Lys  
565

&lt;210&gt; 5

&lt;211&gt; 1841

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;223&gt; M104

&lt;400&gt; 5

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acaaacatgt ttcattgaagc actactacat ggttgccatt cgggtgattt ctgggctcct 1260

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&lt;210&gt; 6

&lt;211&gt; 509

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;223&gt; M104

&lt;400&gt; 6

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Met Ala Ala Glu Gln Gly Arg Ser Leu Ala Glu Thr Pro Thr Trp Ser
  1              5              10              15

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Val Ala Thr Val Thr Thr Leu Met Val Ala Ala Cys Phe Leu Val Glu
          20              25              30

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Arg Ser Leu Ser Arg Phe Ala Lys Trp Leu Arg Lys Thr Lys Arg Lys
      35              40              45

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Ala Met Leu Ala Ala Leu Glu Lys Ile Arg Glu Glu Leu Met Leu Leu
      50              55              60

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```

Gly Val Ile Ser Leu Leu Leu Ser Gln Thr Ala Arg Phe Ile Ser Glu
      65              70              75              80

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```

Ile Cys Val Pro Ser Ser Leu Phe Thr Ser Arg Phe Tyr Ile Cys Ser
          85              90              95

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```

Glu Ser Asp Tyr Gln Asp Leu Leu Arg Asn Thr Asp Ala Asn Gln Thr
      100              105              110

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Ala Leu Asp Lys Asn Met Phe Gly Gly Gln Arg Leu His Val Cys Gly
      115              120              125

```

```

Glu Gly His Glu Pro Phe Val Ser Tyr Glu Gly Leu Glu Gln Leu His
      130              135              140

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Arg Phe Leu Phe Ile Leu Gly Ile Thr His Val Leu Tyr Ser Phe Val

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145		150		155		160
Thr Val Val Leu Ser Met Ile Lys Ile Tyr Ser Trp Arg Lys Trp Glu						
	165		170		175	
Thr Leu Ala Gly Pro Ile Ala Ala Glu Glu Leu Lys Ala Arg Arg Thr						
	180		185		190	
Lys Val Met Arg Arg Gln Ser Thr Phe Val Phe Asn Asn Ala Ser His						
	195		200		205	
Pro Trp Ser Lys Asn Lys Ile Leu Ile Trp Met Leu Cys Phe Leu Arg						
	210		215		220	
Gln Phe Lys Gly Ser Ile Ile Arg Ser Asp Tyr Leu Ala Leu Arg Leu						
	225		230		235	240
Gly Phe Val Thr Tyr His Lys Leu Pro His Ser Tyr Asp Phe His Lys						
	245		250		255	
Tyr Met Val Arg Ser Met Glu Asp Asp Tyr Asn Gly Thr Ile Gly Ile						
	260		265		270	
Ser Trp Pro Leu Trp Ala Tyr Ala Ile Val Cys Ile Leu Ile Asn Val						
	275		280		285	
His Gly Ile Asn Ile Tyr Phe Trp Leu Ser Phe Val Pro Val Ile Leu						
	290		295		300	
Val Leu Leu Val Gly Thr Glu Leu Gln His Val Ile Ala Gln Leu Ala						
	305		310		315	320
Leu Glu Val Ala Glu Ala Thr Ala Pro Tyr Val Gly Ser Gln Leu Lys						
	325		330		335	
Leu Arg Asp Asp Leu Phe Trp Phe Gly Lys Pro Arg Val Leu Trp Trp						
	340		345		350	
Leu Ile Gln Phe Ile Ser Phe Gln Asn Ala Phe Glu Leu Ala Thr Phe						
	355		360		365	
Leu Trp Ser Leu Trp Glu Leu Ser Ala Gln Thr Cys Phe Met Lys His						
	370		375		380	
Tyr Tyr Met Val Ala Ile Arg Leu Ile Ser Gly Leu Leu Val Gln Phe						
	385		390		395	400
Trp Cys Leu Tyr Ser Thr Leu Pro Leu Asn Val Ile Ile Ser Gln Met						

405                      410                      415  
 Gly Ser Lys Phe Lys Lys Ser Leu Val Ser Glu Asn Val Arg Glu Ser  
                     420                      425                      430  
 Leu His Ser Trp Cys Lys Arg Val Lys Asp Arg Ser Arg His Asn Pro  
                     435                      440                      445  
 Leu Phe Ser Arg Asn Gly Thr Leu Thr Thr Arg Ser Val Cys Ser Leu  
                     450                      455                      460  
 Asp Thr Thr Tyr Glu Thr Asp His Glu Thr Asn Thr Val Cys Thr Leu  
                     465                      470                      475                      480  
 Ser Arg Thr Ala Ser Ala Thr Ser Leu Asp Asp Gln Leu Thr Val Val  
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 Thr Val Asp Asp Glu Pro Ser Cys Ile Glu Lys Asp Val  
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 <211> 673  
 <212> DNA  
 <213> Zea mays

<220>  
 <223> Mlo5

<400> 7  
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<210> 8  
 <211> 149  
 <212> PRT  
 <213> Zea mays

&lt;220&gt;

&lt;223&gt; M1o5

&lt;400&gt; 8

Ile His Phe Ile Leu Phe Gln Asn Ala Phe Glu Ile Ala Phe Phe Phe  
 1 5 10 15

Trp Ile Leu Thr Thr Tyr Gly Phe Asn Ser Cys Ile Met Asp His Val  
 20 25 30

Pro Phe Ile Val Pro Arg Leu Val Val Gly Ala Ile Ile Gln Leu Leu  
 35 40 45

Cys Ser Tyr Ser Thr Leu Pro Leu Tyr Ala Ile Val Thr Gln Met Gly  
 50 55 60

Thr Phe Phe Lys Lys Glu Ile Phe Asp Glu His Val Gln Gln Ser Leu  
 65 70 75 80

Leu Gly Trp Ala Gln Lys Ala Lys Lys Arg Lys Ala Leu Arg Asn Asn  
 85 90 95

Gly Asn Gly Ser Asn Gly Ala Ala Ala Gly Ser Ser His Pro Ser Ala  
 100 105 110

Thr Ala Arg Leu Glu Leu Met Arg Arg Ala Val Ala Leu Glu Glu Gly  
 115 120 125

Ser Ala Gly Gly Asn Gly Ser Glu Ala Ser Ala Ala Glu Leu His Asp  
 130 135 140

Thr Gly Pro Lys Leu  
 145

&lt;210&gt; 9

&lt;211&gt; 1815

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;223&gt; M1o6

&lt;400&gt; 9

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 ggcgtgatcg tgctcatctc catcctgctg gagaaggggc tccaccacgt gggcgagttc 180  
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&lt;210&gt; 10

&lt;211&gt; 515

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;223&gt; M106

&lt;400&gt; 10

Met Gly Gly Gly Gly Gly Gly Gly Asn Ser Arg Glu Leu Asp Gln Thr

1 5 10 15

Pro Thr Trp Ala Val Ala Ser Val Cys Gly Val Ile Val Leu Ile Ser

20 25 30

Ile Leu Leu Glu Lys Gly Leu His His Val Gly Glu Phe Phe Ser His

35 40 45

Arg Lys Lys Lys Ala Met Val Glu Ala Leu Glu Lys Val Lys Ala Glu

50 55 60

Leu Met Val Leu Gly Phe Ile Ser Leu Leu Leu Val Phe Gly Gln Asn  
 65 70 75 80  
 Tyr Ile Ile Lys Val Cys Ile Ser Asn His Ala Ala Asn Thr Met Leu  
 85 90 95  
 Pro Cys Lys Leu Glu Ala Ala Ala Val Glu Gly Lys Asp Gly His Gly  
 100 105 110  
 Lys Glu Ala Ala Ala Val Val Ala Gly Lys Lys Lys Val Ala Val Ala  
 115 120 125  
 Val Pro Gly Lys Lys Lys Lys Lys Ala Ala Ala Ala Asp His Leu  
 130 135 140  
 Gly Gly Val Val Asp Trp Pro Pro Pro Tyr Tyr Ala His Asn Ala Arg  
 145 150 155 160  
 Met Leu Ala Glu Ala Ser Met Ala Thr Lys Cys Pro Glu Gly Lys Val  
 165 170 175  
 Pro Leu Ile Ser Ile Asn Ala Leu His Gln Leu His Ile Phe Ile Phe  
 180 185 190  
 Phe Leu Ala Val Phe His Val Ser Tyr Ser Ala Ile Thr Met Ala Leu  
 195 200 205  
 Gly Arg Ala Lys Ile Arg Ala Trp Lys Glu Trp Glu Lys Glu Ala Ala  
 210 215 220  
 Gly Gln Asp Tyr Glu Phe Ser His Asp Pro Thr Arg Phe Arg Phe Thr  
 225 230 235 240  
 His Glu Thr Ser Phe Val Arg Gln His Met Asn Val Leu Asn Lys Phe  
 245 250 255  
 Pro Ala Ser Phe Tyr Ile Ser Asn Phe Phe Arg Gln Phe Phe Arg Ser  
 260 265 270  
 Val Arg Gln Ala Asp Tyr Cys Ala Leu Arg His Ser Phe Val Asn Val  
 275 280 285  
 His Leu Ala Pro Gly Ser Lys Phe Asp Phe Gln Lys Tyr Ile Lys Arg  
 290 295 300  
 Ser Leu Glu Asp Asp Phe Lys Val Ile Val Gly Ile Ser Pro Pro Leu  
 305 310 315 320



Trp Ala Ser Ala Leu Ile Phe Leu Phe Leu Asn Val Asn Gly Trp His  
 325 330 335

Thr Met Leu Trp Ile Ser Ile Met Pro Val Val Ile Ile Leu Ser Val  
 340 345 350

Gly Thr Lys Leu Gln Gly Ile Ile Cys Arg Met Ala Ile Asp Ile Thr  
 355 360 365

Glu Arg His Ala Val Ile Gln Gly Ile Pro Met Val Gln Val Ser Asp  
 370 375 380

Ser Tyr Phe Trp Phe Ala Arg Pro Thr Phe Val Leu Phe Leu Ile His  
 385 390 395 400

Phe Thr Leu Phe Gln Asn Gly Phe Gln Ile Ile Tyr Phe Leu Trp Ile  
 405 410 415

Leu Tyr Glu Tyr Gly Met Asp Ser Cys Phe Asn Asp Ser Glu Glu Phe  
 420 425 430

Val Phe Ala Arg Leu Cys Leu Gly Val Val Val Gln Val Leu Cys Ser  
 435 440 445

Tyr Val Thr Leu Pro Leu Tyr Ala Leu Val Ser Gln Met Gly Ser Thr  
 450 455 460

Met Lys Gln Ser Ile Phe Asp Glu Gln Thr Ser Lys Ala Leu Lys Asn  
 465 470 475 480

Trp Arg Ala Gly Ala Lys Lys Lys Ala Pro Thr Gly Gly Ser Lys His  
 485 490 495

Gly Gly Gly Gly Ser Pro Thr Ala Gly Gly Ser Pro Thr Lys Ala Asp  
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Gly Asp Ala  
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<210> 11

<211> 1660

<212> DNA

<213> Zea mays

<220>

<223> M107

&lt;400&gt; 11

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&lt;210&gt; 12

&lt;211&gt; 499

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;223&gt; M1o7

&lt;400&gt; 12

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Ile Val Cys Leu Val Ile Val Ser Ile Ser Leu Ala Ala Glu Arg Ser
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Leu His Tyr Leu Gly Lys Tyr Leu Glu Cys Lys Lys Gln Lys Ala Leu
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Ile Pro Glu Thr Ser Thr Asp Phe Met Leu Pro Cys Asn Arg Gly Asn  
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Ser Arg Val Ala Glu Glu Gly Ala Lys Ile Cys Asn Lys Lys Gly Asp  
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Val Pro Leu Leu Ser Leu Glu Ala Leu His Gln Leu His Ile Phe Ile  
 115 120 125

Phe Val Leu Gly Leu Val His Val Val Phe Cys Ala Thr Thr Ile Ser  
 130 135 140

Phe Ser Gly Ala Lys Met Arg Lys Trp Lys His Trp Glu Thr Glu Ile  
 145 150 155 160

His Arg Glu Val His Glu Lys Leu Gln Gln Glu Lys Asn Glu Gly Gln  
 165 170 175

Gly Ser Ser Leu Ser Ile Val Val Leu His Arg Glu His Gln Asp Glu  
 180 185 190

Phe Val His Lys Arg Thr Lys Gly Phe Trp Met Lys Leu Ala Val Ala  
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Ser Trp Ile Thr Ala Phe Leu Lys Gln Phe Gln Asp Ser Val Ser Lys  
 210 215 220

Ser Asp Tyr Glu Ala Leu Arg Ser Ala Phe Val Val Glu His Tyr Pro  
 225 230 235 240

Glu Lys Pro Asp Ile Asp Phe His Lys Tyr Met Thr Arg Ala Val Glu  
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Tyr Glu Phe Lys Arg Val Val Gly Ile Ser Trp Tyr Leu Trp Leu Phe  
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Val Ile Leu Phe Leu Leu Leu Asn Ile Asn Gly Trp His Thr Tyr Phe  
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Trp Leu Ala Phe Leu Pro Leu Phe Leu Leu Leu Ile Val Gly Ala Lys  
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 Leu His Gly Phe Gly Ser Arg Val His Glu Ser Val His Gly Trp Ile  
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 Pro Asn Ala Asp Ser Gly Arg Glu Ala Asp Val Thr Arg Arg Val Ala  
 450 455 460  
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<220>  
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&lt;400&gt; 13

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&lt;210&gt; 14

&lt;211&gt; 492

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;223&gt; M108

&lt;400&gt; 14

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Met Ala Ala Glu Gly Glu Ala Ala Ala Leu Glu Phe Thr Pro Thr Trp
  1             5             10             15

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Ile Val Ala Ala Val Cys Ser Leu Ile Val Leu Leu Ser Leu Val Ala
      20             25             30

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Glu Arg Cys Leu His Tyr Leu Gly Lys Thr Leu Lys Arg Lys Asn Gln  
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 Arg Thr Cys Ile Pro Glu Arg Trp Thr Phe His Met Leu Pro Cys Glu  
 85 90 95  
 Lys Pro Asp Glu Lys Ala Gly Glu Ala Ala Thr Met Glu His Phe Val  
 100 105 110  
 Gly Thr Leu Gly Arg Ile Gly Arg Arg Leu Leu Gln Glu Gly Thr Ala  
 115 120 125  
 Gly Ala Glu Gln Cys Gln Lys Lys Gly Lys Val Pro Leu Leu Ser Leu  
 130 135 140  
 Glu Ala Ile His Gln Leu His Ile Phe Ile Phe Val Leu Ala Ile Thr  
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 His Val Ile Phe Ser Val Thr Thr Met Leu Leu Gly Gly Ala Gln Ile  
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 His Gln Trp Lys Gln Trp Glu Asn Gly Ile Lys Lys Asp Ala Pro Gly  
 180 185 190  
 Asn Gly Pro Lys Val Thr Asn Val His His His Glu Phe Ile Lys Lys  
 195 200 205  
 Arg Phe Lys Gly Ile Gly Lys Asp Ser Ile Ile Leu Ser Trp Leu His  
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 Ser Phe Gly Lys Gln Phe Tyr Arg Ser Val Ser Lys Ser Asp Tyr Thr  
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 Thr Met Arg Leu Gly Phe Ile Met Thr His Cys Pro Gly Asn Pro Lys  
 245 250 255  
 Phe Asp Phe His Arg Tyr Met Val Arg Val Leu Glu Ala Asp Phe Lys  
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 Lys Val Val Gly Ile Ser Trp Tyr Leu Trp Val Phe Val Val Ile Phe  
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Leu Leu Leu Asn Val Asn Gly Trp His Thr Tyr Phe Trp Ile Ala Phe  
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Ile Ala Gln Leu Ala His Asp Val Ala Glu Lys His Thr Ala Val Glu  
 325 330 335

Gly Asp Val Ile Val Lys Pro Ser Asp Glu His Phe Trp Phe Gly Lys  
 340 345 350

Pro Arg Val Ile Leu Tyr Leu Ile His Phe Ile Leu Phe Gln Asn Ala  
 355 360 365

Phe Glu Ile Ala Phe Phe Phe Trp Ile Leu Ser Thr Tyr Gly Phe Asp  
 370 375 380

Ser Cys Ile Met Gly Gln Val Arg Phe Ile Val Pro Arg Leu Val Ile  
 385 390 395 400

Gly Val Val Ile Gln Leu Leu Cys Ser Tyr Ser Thr Leu Pro Leu Tyr  
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Ala Ile Val Thr Gln Met Gly Ser Cys Tyr Lys Lys Glu Ile Phe Asn  
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Glu His Val Gln Gln Gly Val Leu Gly Trp Ala Gln Lys Val Lys Met  
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Lys Lys Gly Leu Lys Gly Ala Ala Ser Ala Ser Lys Asp Glu Ser Ile  
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<212> DNA

<213> Zea mays

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<223> M109

&lt;400&gt; 15

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&lt;210&gt; 16

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;223&gt; Mlo9

&lt;400&gt; 16

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  1             5             10             15

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Cys Arg Glu Gly Tyr Glu Ser Phe Val Ser His Glu Gly Leu Glu Gln
      20             25             30

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Leu His Arg Phe Ile Phe Val Met Ala Val Thr His Val Thr Tyr Ser
    35             40             45

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Cys Leu Thr Met Leu Leu Ala Ile Leu Lys Ile His Lys Trp Arg Lys
    50             55             60

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 Ser Phe Arg Ser Trp Ser Gln Asn Asn Val Val Met Trp Leu Val Cys  
 100 105 110  
 Phe Ile Ala Gln Phe Gly Gln Ser Val Val Arg Ala Asp Tyr Leu Ile  
 115 120 125  
 Leu Arg Lys Gly Phe Ile Met Thr His Asn Leu Pro Pro Thr Tyr Asp  
 130 135 140  
 Phe His Asn Tyr Met Ile Arg Ser Met Glu Glu Glu Phe Glu Lys Ile  
 145 150 155 160  
 Val Gly Val Ser Gly Leu Leu Trp Gly Phe Val Val Ala Phe Met Leu  
 165 170 175  
 Phe Asn Val Asp Gly Ser Asn Leu Tyr Phe Trp Ile Ala Ile Leu Pro  
 180 185 190  
 Val Thr Leu Val Leu Leu Val Gly Ala Lys Leu Gln His Val Ile Ala  
 195 200 205  
 Thr Leu Thr Ala Glu Gly Ala Lys Met Ser Thr Tyr Gly Pro Arg Ile  
 210 215 220  
 Gln Pro Arg Asp Asp Leu Phe Trp Phe Lys Lys Pro Glu Phe Leu Leu  
 225 230 235 240  
 Trp Leu Ile His Phe Val Leu Phe Gln Asn Ala Phe Glu Leu Ala Ser  
 245 250 255  
 Phe Phe Trp Phe Trp Trp Gln Phe Gly Tyr Asp Ser Cys Phe Ile Lys  
 260 265 270  
 Asn His Leu Leu Val Tyr Cys Arg Leu Ile Leu Gly Phe Ala Gly Gln  
 275 280 285  
 Phe Leu Cys Ser Tyr Ser Thr Leu Pro Val Tyr Ala Leu Val Thr Gln  
 290 295 300  
 Met Gly Ser Lys Tyr Lys Ala Ala Leu Ile Pro Arg Arg Ile Arg Glu  
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Thr Ile His Gly Trp Gly Lys Ala Thr Arg Lys Lys Arg Arg Arg Arg  
 325 330 335

Arg Gly Asp Asp Ser Thr Val Arg Thr Glu Thr Ser Thr Val Cys Ser  
 340 345 350

Leu Thr Asp Asp Asp Glu Asp Phe Glu Asp Asp Asp Asp His His His  
 355 360 365

His Gly Pro Ser Tyr Asp Thr Pro Arg Ala Gly Gly Arg Pro Pro Tyr  
 370 375 380

Leu Lys Ile Glu Thr His Arg Gln Ser Gly Ser Gly His Asp Gly Pro  
 385 390 395 400

Arg Pro Gly Gly Thr Pro Cys Phe His Pro Ser Gly Ser Gly Ser Gly  
 405 410 415

His Ala Met Leu Leu Arg Gln Ala Ser Val Ser Ala Pro Ser Ser Pro  
 420 425 430

Ser Tyr Arg Gly Gly Asn Asn Val Thr Arg Ser Ala Ser Met Pro Gly  
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Ile Ala Ala Leu Arg Thr Thr Gly Ser Gly Thr Pro Thr Arg Val Ser  
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His Glu Glu Pro Thr  
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<210> 17

<211> 533

<212> PRT

<213> Hordeum vulgare

<400> 17

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Leu Met Glu His Gly Leu His Lys Leu Gly His Trp Phe Gln His Arg  
 35 40 45

His Lys Lys Ala Leu Trp Glu Ala Leu Glu Lys Met Lys Ala Glu Leu

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65	70	75 80
Ile Ile Ala Lys Ile Cys Ile Ser Glu Asp Ala Ala Asp Val Met Trp		
	85	90 95
Pro Cys Lys Arg Gly Thr Glu Gly Arg Lys Pro Ser Lys Tyr Val Asp		
	100	105 110
Tyr Cys Pro Glu Gly Lys Val Ala Leu Met Ser Thr Gly Ser Leu His		
	115	120 125
Gln Leu His Val Phe Ile Phe Val Leu Ala Val Phe His Val Thr Tyr		
	130	135 140
Ser Val Ile Thr Ile Ala Leu Ser Arg Leu Lys Met Arg Thr Trp Lys		
	145	150 155 160
Lys Trp Glu Thr Glu Thr Thr Ser Leu Glu Tyr Gln Phe Ala Asn Asp		
	165	170 175
Pro Ala Arg Phe Arg Phe Thr His Gln Thr Ser Phe Val Lys Arg His		
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Leu Gly Leu Ser Ser Thr Pro Gly Ile Arg Trp Val Val Ala Phe Phe		
	195	200 205
Arg Gln Phe Phe Arg Ser Val Thr Lys Val Asp Tyr Leu Thr Leu Arg		
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Ala Gly Phe Ile Asn Ala His Leu Ser Gln Asn Ser Lys Phe Asp Phe		
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His Lys Tyr Ile Lys Arg Ser Met Glu Asp Asp Phe Lys Val Val Val		
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	275	280 285
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	290	295 300
Met Ala Leu Glu Ile Gln Asp Arg Ala Ser Val Ile Lys Gly Ala Pro		

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 Val Val Ala His Pro Val His Arg Leu Asn Pro Asn Asp Arg Arg Arg  
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
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<210> 19

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide  
primer

<400> 19

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28

<210> 20

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide primer

<400> 20

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32

# INTERNATIONAL SEARCH REPORT

Int. onal Application No  
PCT/US 99/15255

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C07K14/415 C12N15/82 A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K C12N A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 04586 A (INNES JOHN CENTRE INNOV LTD ;PANSTRUGA RALPH (GB); BUESCHGES RAINE) 5 February 1998 (1998-02-05) the whole document	1-11, 13-17
X	DATABASE EMBL Online! EMBL AC/ID AA660856, 14 November 1997 (1997-11-14) COVITZ P A ET AL.: "Expressed sequence tags from a root hair-enriched Medicago trunculata cDNA library" XP002119426 abstract	13

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

19 October 1999

Date of mailing of the international search report

03/11/1999

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